

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2003, 23:56:24 ; Search time 8 Seconds  
(without alignments)  
1027.619 Million cell updates/sec

Title: US-09-877-633-2

Perfect score: 2028

Sequence: 1 caaaaggaagaataataaa.....agtagacagtgatgga 2028

Scoring table: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched: 5275 seqs, 2026861 residues

Total number of hits satisfying chosen parameters: 10550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 350 summaries

Database :

EMBL\_EST.\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estnu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_estfun.\*

9: em\_estom.\*

10: em\_hic.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	35.6	1.8	308	9	Bi040900 MI-P-NA-a
C 2	35.2	1.7	659	3	AU212636 Caenorhab
C 3	32.6	1.6	195	9	Bf713200 MI-P-O2-a
C 4	32.2	1.6	465	9	Bi006626 MI-P-AY1-
C 5	31.4	1.5	259	9	Bf702228 MI-P-A2-a
C 6	31.4	1.5	500	2	Bm740200 K-EST0011
C 7	31.4	1.5	556	9	Bf702953 MI-P-H1-a
C 8	31.2	1.5	136	2	HS0010501
C 9	31.2	1.5	374	9	Bf712847 MI-P-O1-a
C 10	31	1.5	472	2	HS0002682
C 11	30.8	1.5	400	9	Bf712218 MI-P-A3-a
C 12	30.6	1.5	502	9	Bf703505 MI-P-H1-a
C 13	30.2	1.5	321	6	BQ236337 TaE05035A
C 14	30.2	1.5	512	9	Bf713152 MI-P-O1-a
C 15	30	1.5	273	2	HS0002678
C 16	29.8	1.5	300	9	Bf711870 MI-P-O3-a
C 17	29.6	1.5	127	2	HS0010205
C 18	29.4	1.4	147	2	HS0003359
C 19	29.4	1.4	150	9	Bf711427 MI-P-A2-a
C 20	29.4	1.4	414	9	Bf712867 MI-P-O1-a
C 21	29.4	1.4	417	9	Bf704037 MI-P-A3-a
C 22	29.2	1.4	144	2	HS0001232
C 23	29.2	1.4	206	9	Bf713586 MI-P-O2-a

C 24	29.2	1.4	306	9	Bi040658
C 25	29.2	1.4	385	9	Bf703246
C 26	29.2	1.4	422	6	Bm377646 EBem04_SQ
C 27	29.2	1.4	445	9	Bf711499 MI-P-A2-a
C 28	29	1.4	311	9	Bf702714 MI-P-E3-a
C 29	29	1.4	412	9	Bf713046 MI-P-H3-a
C 30	29	1.4	428	9	Bf704356 MI-P-O3-a
C 31	29	1.4	576	9	Bi400750 MI-P-AY1-
C 32	28.8	1.4	130	2	HS0005765
C 33	28.8	1.4	137	2	HS0002748
C 34	28.8	1.4	197	9	Bf709714 MI-P-AV1-
C 35	28.8	1.4	313	9	Bf709877 MI-P-AV1-
C 36	28.6	1.4	115	2	HS0010170
C 37	28.6	1.4	277	2	HS0004384
C 38	28.6	1.4	288	9	Bf703566 MI-P-H1-a
C 39	28.6	1.4	391	9	Bf704175 MI-P-O3-a
C 40	28.4	1.4	112	2	HS0001422
C 41	28.4	1.4	245	9	Bf703358 MI-P-O3-a
C 42	28.4	1.4	273	9	Bf708447 MI-P-AV0-
C 43	28.4	1.4	422	6	Bm377646 EBem04_SQ
C 44	28.2	1.4	129	2	HS0011693
C 45	28	1.4	131	2	HS0010495
C 46	28	1.4	308	9	Bf713343 MI-P-O2-a
C 47	28	1.4	331	6	Bm444148 EBem09_SQ
C 48	28	1.4	348	3	AU209841 Caenorhab
C 49	28	1.4	498	2	Bm832939 K-EST0107
C 50	28	1.4	522	9	Bf713161 MI-P-O1-a
C 51	27.8	1.4	337	9	Bf702115 MI-P-A1-a
C 52	27.8	1.4	343	2	HSC9743
C 53	27.8	1.4	460	6	Bm099974 EBes01_SQ
C 54	27.8	1.4	716	3	AU2117241 Caenorhab
C 55	27.6	1.4	124	2	HS0010444
C 56	27.6	1.4	284	9	Bf703336 MI-P-A3-a
C 57	27.6	1.4	348	2	HS0002737
C 58	27.6	1.4	444	6	Bm378023 EBem04_SQ
C 59	27.6	1.4	522	9	Bi400734 MI-P-AY1-
C 60	27.6	1.4	569	2	Bm818575 K-EST0085
C 61	27.6	1.4	647	2	HS0003964
C 62	27.6	1.4	798	2	HS000364
C 63	27.4	1.4	125	2	HS0001209
C 64	27.4	1.4	142	2	HS0003075
C 65	27.4	1.4	380	9	Bf711490 MI-P-O3-a
C 66	27.4	1.4	402	6	Bm372823 EBma04_SQ
C 67	27.4	1.4	437	6	Bm370203 EBRO08_SQ
C 68	27.4	1.4	604	2	Bm854730 K-EST0137
C 69	27.4	1.4	680	2	HS0002724
C 70	27.2	1.3	269	9	Bf703694 MI-P-E4-a
C 71	27.2	1.3	382	2	HSC2714
C 72	27.2	1.3	571	3	AU218039 Human Heart
C 73	27	1.3	125	2	HS0010819
C 74	27	1.3	125	2	HS0002746
C 75	27	1.3	649	9	Bf703011 MI-P-E5-a
C 76	26.8	1.3	120	2	HS0010864
C 77	26.8	1.3	128	2	HS0010497
C 78	26.8	1.3	139	2	HS0001338
C 79	26.8	1.3	147	2	HS0002744
C 80	26.8	1.3	224	9	Bf703629 MI-P-H1-a
C 81	26.8	1.3	361	2	HS0003968
C 82	26.8	1.3	445	9	Bi400057 MI-P-AV1-
C 83	26.8	1.3	454	2	HS0011933
C 84	26.8	1.3	469	9	Bf711270 MI-P-O3-a
C 85	26.8	1.3	498	2	Bm856410 X-EST0140
C 86	26.6	1.3	110	2	HS0004754
C 87	26.6	1.3	124	9	Bf702532 MI-P-E3-a
C 88	26.6	1.3	127	2	HS0010835
C 89	26.6	1.3	217	9	Bf703980 MI-P-O1-a
C 90	26.6	1.3	240	9	Bf713193 MI-P-O1-a
C 91	26.6	1.3	300	9	Bf709445 MI-P-AY0-
C 92	26.6	1.3	346	9	Bf710556 MI-P-AV1-
C 93	26.6	1.3	352	9	Bf711589 MI-P-A1-a
C 94	26.6	1.3	366	9	Bf711564 MI-P-A2-a
C 95	26.6	1.3	443	6	Bm374465 EBp103_SQ
C 96	26.6	1.3	446	9	Bf702796 MI-P-H3-a

97	26.6	1.3	451	2	HSM004354	Al039878 Homo sapi	C 170	25.2	1.2	409	2	BM856839	HM856839 K-EST0140
98	26.6	1.3	485	2	BM856662	BM856662 K-EST0140	C 171	25.2	1.2	431	9	BF703269	BF703269 MI-P-A3-a
99	26.6	1.3	609	2	HSM002666	Al038323 Homo sapi	C 172	25.2	1.2	451	9	BF702085	BF702085 MI-P-A1-a
100	26.6	1.3	672	2	BM851675	BM851675 K-EST0132	C 173	25.2	1.2	453	2	AF120351	AF120351 Homo sapi
101	26.4	1.3	114	2	HSM010848	Al045958 Homo sapi	C 174	25.2	1.2	582	2	BM738713	BM738713 K-EST0006
102	26.4	1.3	129	2	HSM005730	Al041254 Homo sapi	C 175	25.2	1.2	597	6	BM734584	BM734584 EBma05 SQ
103	26.4	1.3	288	9	BF703718	BF703718 MI-P-E4-a	C 176	25.2	1.2	632	3	AU217172	AU217172 Caenorhab
104	26.4	1.3	351	9	BF710483	BF710483 MI-P-AY1-	C 177	25	1.2	64	2	HSM002423	Al038084 Homo sapi
105	26.4	1.3	439	2	AF119319	AF119319 Homo sapi	C 178	25	1.2	84	2	HSM002938	Al038462 Homo sapi
106	26.4	1.3	446	2	BM830489	BM830489 K-EST0104	C 179	25	1.2	118	2	HSM002462	Al038123 Homo sapi
107	26.4	1.3	454	2	AF119566	AF119566 Homo sapi	C 180	25	1.2	138	9	BF709622	BF709622 MI-P-AY0-
108	26.4	1.3	536	9	BF713165	BF713165 MI-P-O1-a	C 181	25	1.2	151	2	HSM002734	Al038388 Homo sapi
109	26.4	1.3	536	9	BF713165	BF713165 MI-P-O1-a	C 182	25	1.2	151	2	HSM002734	Al038388 Homo sapi
110	26.4	1.3	536	9	BF713165	BF713165 MI-P-O1-a	C 183	25	1.2	151	2	HSM002734	Al038388 Homo sapi
111	26.2	1.3	156	2	HSM002751	Al038405 Homo sapi	C 184	25	1.2	272	9	BI400524	BI400524 MI-P-AY1-
112	26.2	1.3	233	9	BI400101	BI400101 MI-P-AY1-	C 185	25	1.2	272	9	BI400593	BI400593 MI-P-AY1-
113	26.2	1.3	311	9	BI400269	BI400269 MI-P-AY1-	C 186	25	1.2	381	2	BM823395	BM823395 K-EST0094
114	26.2	1.3	377	9	BF712991	BF712991 MI-P-O2-a	C 187	25	1.2	389	9	BF712307	BF712307 MI-P-A3-a
115	26.2	1.3	448	9	BF702426	BF702426 MI-P-A2-a	C 188	25	1.2	400	6	BQ241093	BQ241093 TAE05009C
116	26.2	1.3	498	2	BM856410	BM856410 K-EST0140	C 189	25	1.2	426	9	BF703733	BF703733 MI-P-E4-a
117	26.2	1.3	512	6	BQ236750	BQ236750 TAE05027D	C 190	25	1.2	428	9	BF703873	BF703873 MI-P-O1-a
118	26.2	1.3	571	9	BF702348	BF702348 MI-P-A2-a	C 191	25	1.2	452	9	BF702344	BF702344 MI-P-A2-a
119	26	1.3	124	2	HSM010174	Al045324 Homo sapi	C 192	25	1.2	652	2	HSM002696	BM835653 K-EST0110
120	26	1.3	139	2	HSM0011341	Al037017 Homo sapi	C 193	25	1.2	61	2	HSM011387	Al038352 Homo sapi
121	26	1.3	144	2	HSM0011210	Al036893 Homo sapi	C 194	24.8	1.2	102	2	HSM011387	Al045831 Homo sapi
122	26	1.3	230	6	BM445013	BM445013 EBem09 SQ	C 195	24.8	1.2	110	2	HSM010681	Al045831 Homo sapi
123	26	1.3	270	9	BF702005	BF702005 MI-P-A1-a	C 196	24.8	1.2	118	9	BF703409	BF703409 MI-P-O3-a
124	26	1.3	366	9	BF712209	BF712209 MI-P-E4-a	C 197	24.8	1.2	133	2	HSM004867	Al043991 Homo sapi
125	26	1.3	423	9	BI404717	BI404717 MI-P-NA-a	C 198	24.8	1.2	255	2	AF119299	AF119299 Homo sapi
126	26	1.3	438	2	BM853947	BM853947 K-EST0136	C 199	24.8	1.2	255	2	AF119300	AF119300 Homo sapi
127	26	1.3	451	2	AF120342	AF120342 Homo sapi	C 200	24.8	1.2	331	9	BF704028	BF704028 MI-P-A3-a
128	26	1.3	550	2	BM850757	BM850757 K-EST0131	C 201	24.8	1.2	351	9	BF710483	BF710483 MI-P-AY1-
129	26	1.3	572	6	BQ237294	BQ237294 TAE05019B	C 202	24.8	1.2	370	6	BM099840	BM099840 EBem01 SQ
130	26	1.3	574	2	BM833156	BM833156 K-EST0107	C 203	24.8	1.2	389	6	BM778083	BM778083 EBem07 SQ
131	26	1.3	603	6	BQ240324	BQ240324 TAE05019B	C 204	24.8	1.2	432	9	BF703444	BF703444 MI-P-H1-a
132	25.8	1.3	1133	2	HSM007179	Al042329 Homo sapi	C 205	24.8	1.2	433	6	BM370064	BM370064 EBem08 SQ
133	25.8	1.3	97	2	HSM002694	Al038350 Homo sapi	C 206	24.8	1.2	439	6	BM376642	BM376642 EBem05 SQ
134	25.8	1.3	125	9	BF709090	BF709090 MI-P-AY0-	C 207	24.8	1.2	461	6	BM097368	BM097368 EBem01 SQ
135	25.8	1.3	233	9	BF711163	BF711163 MI-P-AY1-	C 208	24.8	1.2	476	6	BM441946	BM441946 EBem01 SQ
136	25.8	1.3	324	9	BF703778	BF703778 MI-P-E4-a	C 209	24.8	1.2	509	9	BI404683	BI404683 MI-P-NA-a
137	25.8	1.3	340	9	BF702922	BF702922 MI-P-H2-a	C 210	24.8	1.2	515	2	BM829919	BM829919 K-EST0103
138	25.8	1.3	430	6	BM377494	BM377494 EBem04 SQ	C 211	24.8	1.2	535	2	BM836836	BM836836 K-EST0112
139	25.8	1.3	441	6	BM377494	BM377494 TAE05037B	C 212	24.8	1.2	556	2	BM833127	BM833127 K-EST0107
140	25.8	1.3	572	6	BQ236179	BQ236179 TAE05037B	C 213	24.8	1.2	617	2	BM827422	BM827422 K-EST0099
141	25.8	1.3	597	2	BM782406	BM782406 K-EST0059	C 214	24.8	1.2	632	6	BQ238563	BQ238563 TAE05002E
142	25.8	1.3	652	2	HSM001625	Al037299 Homo sapi	C 215	24.8	1.2	705	2	BM787544	BM787544 K-EST0110
143	25.6	1.3	143	2	HSM002494	Al038155 Homo sapi	C 216	24.8	1.2	705	2	BM787544	BM787544 K-EST0110
144	25.6	1.3	288	9	BF703566	BF703566 MI-P-H1-a	C 217	24.8	1.2	103	2	HSM001297	Al036974 Homo sapi
145	25.6	1.3	292	6	BM443562	BM443562 EBem02 SQ	C 218	24.8	1.2	107	2	HSM002922	Al038446 Homo sapi
146	25.6	1.3	356	9	BF711582	BF711582 MI-P-A1-a	C 219	24.6	1.2	109	2	HSM001301	Al036978 Homo sapi
147	25.6	1.3	357	6	BM098386	BM098386 EBem08 SQ	C 220	24.6	1.2	126	2	HSM005648	Al038557 Homo sapi
148	25.6	1.3	380	9	BF713194	BF713194 MI-P-O1-a	C 221	24.6	1.2	133	2	HSM0003063	BF709088 MI-P-AY0-
149	25.6	1.3	441	6	BM369984	BM369984 EBem08 SQ	C 222	24.6	1.2	206	9	BF709088	BF709088 MI-P-AY0-
150	25.6	1.3	468	2	BM856544	BM856544 K-EST0140	C 223	24.6	1.2	255	2	AF119298	AF119298 Homo sapi
151	25.6	1.3	536	5	BQ109625	BQ109625 imagec 9	C 224	24.6	1.2	309	6	BQ240344	BQ240344 TAE05018H
152	25.6	1.3	587	2	BM793473	BM793473 K-EST0074	C 225	24.6	1.2	334	6	BM371424	BM371424 EBma08 SQ
153	25.4	1.3	93	2	HSM002749	Al038403 Homo sapi	C 226	24.6	1.2	356	9	BF713064	BF713064 MI-P-H3-a
154	25.4	1.3	306	9	BI404658	BI404658 MI-P-NA-a	C 227	24.6	1.2	416	9	BF702792	BF702792 MI-P-H3-a
155	25.4	1.3	347	6	BM101379	BM101379 EBem01 SQ	C 228	24.6	1.2	420	2	BM752420	BM752420 K-EST0028
156	25.4	1.3	416	9	BF712777	BF712777 MI-P-H1-a	C 229	24.6	1.2	442	2	AF119298	AF119298 Homo sapi
157	25.4	1.3	426	9	BF704519	BF704519 MI-P-H4-a	C 230	24.6	1.2	459	2	AF119565	AF119565 Homo sapi
158	25.4	1.3	446	9	BF701919	BF701919 MI-P-E3-a	C 231	24.6	1.2	490	9	BF713184	BF713184 MI-P-O1-a
159	25.4	1.3	461	2	HSM002758	Al038412 Homo sapi	C 232	24.6	1.2	494	3	AU217784	AU217784 Caenorhab
160	25.4	1.3	481	6	BM441017	BM441017 EBem02 SQ	C 233	24.6	1.2	502	9	BF709088	BF709088 MI-P-AY1-
161	25.4	1.3	484	9	BF711440	BF711440 MI-P-A2-a	C 234	24.6	1.2	514	3	AU217052	AU217052 Caenorhab
162	25.4	1.3	511	9	BF700531	BF700531 MI-P-AY1-	C 235	24.6	1.2	517	9	BF709457	BF709457 MI-P-AY0-
163	25.2	1.2	595	3	AU221564	AU221564 Caenorhab	C 236	24.6	1.2	669	3	HSM003105	Al038629 Homo sapi
164	25.2	1.2	74	2	HSM003089	Al038613 Homo sapi	C 237	24.6	1.2	90	2	HSM010752	BF709082 MI-P-AY0-
165	25.2	1.2	80	2	HSM003090	Al038613 Homo sapi	C 238	24.6	1.2	110	2	HSM010752	BF709082 MI-P-AY0-
166	25.2	1.2	97	2	HSM001884	Al037553 Homo sapi	C 239	24.4	1.2	123	2	HSM002918	Al038442 Homo sapi
167	25.2	1.2	113	2	HSM002662	Al038319 Homo sapi	C 240	24.4	1.2	133	2	HSM002918	Al038442 Homo sapi
168	25.2	1.2	190	9	BF704023	BF704023 MI-P-A3-a	C 241	24.4	1.2				
169	25.2	1.2	245	9	BF709664	BF709664 MI-P-AY0-	C 242	24.4	1.2				
			398	9	BF702734	BF702734 MI-P-E3-a							

243	24.4	1.2	163	9	Bf713226	MI-P-O1-a	Bf713226	MI-P-O1-a	C 316	24	1.2	447	2	AF119559	Homo sapi
244	24.4	1.2	265	9	Bf1399011	MI-P-AV1-	Bi399011	MI-P-AV1-	317	24	1.2	448	9	Bf711461	MI-P-O3-a
c 245	24.4	1.2	283	3	AU216457	Caenorhab	Au216457	Caenorhab	318	24	1.2	453	9	Bf713178	MI-P-O1-a
246	24.4	1.2	298	9	Bf401983	MI-P-CP0-	Bi401983	MI-P-CP0-	319	24	1.2	458	2	AF120341	Homo sapi
247	24.4	1.2	340	9	Bf710205	MI-P-AV1-	Bf710205	MI-P-AV1-	320	24	1.2	464	2	AF120354	Homo sapi
c 248	24.4	1.2	345	9	Bi404800	MI-P-H5-a	Bi404800	MI-P-H5-a	c 321	24	1.2	497	9	Bi400892	MI-P-AV1-
249	24.4	1.2	347	9	Bf709485	MI-P-AV0-	Bf709485	MI-P-AV0-	c 322	24	1.2	511	9	Bi400531	MI-P-AV1-
c 250	24.4	1.2	355	9	Bf704170	MI-P-O3-a	Bf704170	MI-P-O3-a	323	24	1.2	514	6	BQ240147	TaE05021E
c 251	24.4	1.2	358	6	Bf779820	EBem07_SQ	Bi779820	EBem07_SQ	324	24	1.2	523	2	BM739652	K-EST0009
c 252	24.4	1.2	375	9	Bf709762	MI-P-AV0-	Bf709762	MI-P-AV0-	325	24	1.2	563	2	HSW004571	Homo sapi
c 253	24.4	1.2	436	2	BM854830	K-EST0137	BM854830	K-EST0137	c 326	24	1.2	570	2	Bf711476	MI-P-O3-a
254	24.4	1.2	438	6	BM099169	EBem01_SQ	BM099169	EBem01_SQ	c 327	24	1.2	570	2	BM854872	K-EST0137
255	24.4	1.2	441	6	BM375590	EBem06_SQ	BM375590	EBem06_SQ	c 328	24	1.2	628	9	Bf713187	MI-P-O1-a
256	24.4	1.2	442	6	BM099642	EBem01_SQ	BM099642	EBem01_SQ	329	23.8	1.2	70	2	HSW010676	Homo sapi
257	24.4	1.2	454	2	AF119566	Homo sapi	AF119566	Homo sapi	330	23.8	1.2	91	2	HSW011994	Homo sapi
c 258	24.4	1.2	461	2	AF120340	Homo sapi	AF120340	Homo sapi	331	23.8	1.2	103	2	HSW010743	Homo sapi
c 259	24.4	1.2	502	2	HSW004322	Homo sapi	AF103846	Homo sapi	332	23.8	1.2	112	2	HSW011301	Homo sapi
c 260	24.4	1.2	506	9	Bf704422	MI-P-E6-a	Bf704422	MI-P-E6-a	c 333	23.8	1.2	119	2	HSW003284	Homo sapi
261	24.4	1.2	618	2	BM853322	K-EST0136	BM853322	K-EST0136	c 334	23.8	1.2	134	2	HSW001164	Homo sapi
262	24.4	1.2	650	2	BM827765	K-EST0100	BM827765	K-EST0100	335	23.8	1.2	142	2	HSW002924	Homo sapi
263	24.4	1.2	651	2	BM829019	K-EST0101	BM829019	K-EST0101	336	23.8	1.2	167	9	Bf704551	MI-P-H4-a
264	24.2	1.2	107	2	HSW010727	Homo sapi	Al045877	Homo sapi	337	23.8	1.2	179	9	Bf708579	MI-P-AV0-
265	24.2	1.2	108	2	HSW003026	Homo sapi	Al038550	Homo sapi	338	23.8	1.2	206	9	Bf713586	MI-P-O2-a
266	24.2	1.2	122	2	HSW002679	Homo sapi	Al038336	Homo sapi	c 339	23.8	1.2	253	2	HSW002762	Homo sapi
267	24.2	1.2	131	2	HSW011320	Homo sapi	Al046470	Homo sapi	c 340	23.8	1.2	257	9	Bi400793	MI-P-AV1-
268	24.2	1.2	135	2	HSW002756	Homo sapi	Al038410	Homo sapi	c 341	23.8	1.2	265	9	Bi399011	MI-P-AV1-
269	24.2	1.2	151	9	Bi399411	MI-P-AV1-	Bi399411	MI-P-AV1-	c 342	23.8	1.2	269	9	Bf704128	MI-P-O1-a
c 270	24.2	1.2	174	9	Bf710762	MI-P-AV1-	Bf710762	MI-P-AV1-	c 343	23.8	1.2	270	2	HSC5696	Human Heart
c 271	24.2	1.2	333	9	Bf712166	MI-P-E6-a	Bf712166	MI-P-E6-a	c 344	23.8	1.2	277	2	HSW004384	Homo sapi
c 272	24.2	1.2	336	2	HSC6892	Human Heart	CO4689	Human Heart	c 345	23.8	1.2	286	9	Bf713516	MI-P-E3-a
c 273	24.2	1.2	345	9	Bf702107	MI-P-A1-a	Bf702107	MI-P-A1-a	346	23.8	1.2	307	9	Bf713181	MI-P-O1-a
c 274	24.2	1.2	368	2	HSC3975	Human Heart	CO5397	Human Heart	c 347	23.8	1.2	310	2	BM835906	K-EST0111
c 275	24.2	1.2	379	2	HSC4704	Human Heart	CO4470	Human Heart	c 348	23.8	1.2	342	9	Bi399743	MI-P-AV1-
c 276	24.2	1.2	388	2	HSC4045	Human Heart	CO5404	Human Heart	c 349	23.8	1.2	354	9	Bf701908	MI-P-E3-a
c 277	24.2	1.2	393	9	Bf711193	MI-P-E6-a	Bf711193	MI-P-E6-a	350	23.8	1.2	372	6	BM369980	EBro08_SQ
278	24.2	1.2	399	6	BM369181	EBem07_SQ	BM369181	EBem07_SQ	ALIGNMENTS						
c 279	24.2	1.2	402	2	HSC7862	Human Heart	CO2786	Human Heart	RESULT 1						
c 280	24.2	1.2	416	9	Bf704396	MI-P-E6-a	Bi704396	MI-P-E6-a	BI404900/c	standard; RNA; EST; 308 BP.					
c 281	24.2	1.2	440	6	Bf779326	EBro01_SQ	Bi779326	EBro01_SQ	ID BI404900						
c 282	24.2	1.2	444	6	BM374457	EBp103_SQ	BM374457	EBp103_SQ	XX						
c 283	24.2	1.2	449	2	HSDEH0056	H. sapienE	Z26977	H. sapienE	AC						
c 284	24.2	1.2	457	6	BQ236739	TaE05027E	BQ236739	TaE05027E	XX						
c 285	24.2	1.2	494	2	BM837856	K-EST0114	BM837856	K-EST0114	SV						
c 286	24.2	1.2	503	2	AF119561	Homo sapi	AF119561	Homo sapi	DT						
c 287	24.2	1.2	522	2	Bf768743	K-EST0051	BM768743	K-EST0051	XX						
c 288	24.2	1.2	601	2	HSW011999	Homo sapi	Al047149	Homo sapi	DT						
c 289	24.2	1.2	623	3	AU212829	Caenorhab	Au212829	Caenorhab	DE						
c 290	24.2	1.2	665	3	AU214507	Caenorhab	Au214507	Caenorhab	XX						
c 291	24.2	1.2	671	6	BG908649	TaLx1170B	Bg908649	TaLx1170B	KW						
c 292	24.2	1.2	679	2	HSW004268	Homo sapi	Al039792	Homo sapi	XX						
c 293	24.2	1.2	694	3	AU218691	Caenorhab	Au218691	Caenorhab	OS						
c 294	24.2	1.2	753	3	AU217453	Caenorhab	Au217453	Caenorhab	XX						
c 295	24.2	1.2	798	2	HSW004616	Homo sapi	Al040140	Homo sapi	XX						
296	24	1.2	92	2	HSW010774	Homo sapi	Al045924	Homo sapi	XX						
c 297	24	1.2	102	2	HSW010480	Homo sapi	Al045630	Homo sapi	XX						
c 298	24	1.2	153	3	AU217183	Caenorhab	Au217183	Caenorhab	OS						
c 299	24	1.2	161	9	Bf711317	MI-P-A1-a	Bf711317	MI-P-A1-a	XX						
300	24	1.2	184	9	Bf708956	MI-P-AV0-	Bf708956	MI-P-AV0-	XX						
301	24	1.2	196	9	Bf712210	MI-P-E4-a	Bf712210	MI-P-E4-a	XX						
302	24	1.2	246	9	Bf711496	MI-P-A2-a	Bi711496	MI-P-A2-a	XX						
303	24	1.2	249	6	Bi777589	EBro04_SQ	Bi777589	EBro04_SQ	XX						
c 304	24	1.2	268	9	Bf708508	MI-P-AV0-	Bf708508	MI-P-AV0-	XX						
c 305	24	1.2	270	9	Bf709379	MI-P-AV0-	Bf709379	MI-P-AV0-	XX						
306	24	1.2	279	6	BM371293	EBma08_SQ	BM371293	EBma08_SQ	XX						
c 307	24	1.2	315	9	Bi4000119	MI-P-AV1-	Bi4000119	MI-P-AV1-	XX						
c 308	24	1.2	322	9	Bf702047	MI-P-A1-a	Bf702047	MI-P-A1-a	XX						
c 309	24	1.2	380	2	AF121329	Homo sapi	AF121329	Homo sapi	XX						
c 310	24	1.2	385	9	Bf703427	MI-P-H1-a	Bf703427	MI-P-H1-a	XX						
c 311	24	1.2	385	9	Bf703704	MI-P-E4-a	Bf703704	MI-P-E4-a	XX						
c 312	24	1.2	391	9	Bf704458	MI-P-E6-a	Bf704458	MI-P-E6-a	XX						
c 313	24	1.2	393	6	Bi779723	EBem05_SQ	Bi779723	EBem05_SQ	XX						
c 314	24	1.2	415	9	Bf709503	MI-P-AV0-	Bi709503	MI-P-AV0-	XX						
315	24	1.2	444	6	BM443476	EBro02_SQ	BM443476	EBro02_SQ	XX						

CONTACT: TUGGLE CK  
MOLECULAR GENETICS LABORATORY, DEPARTMENT OF ANIMAL SCIENCE  
IOWA STATE UNIVERSITY

CC 201 Kildee Hall, Ames, IA 50011-3150, USA  
CC Tel: 5152944252  
CC Fax: 5152942401  
CC Email: kttuggle@iastate.edu  
CC The sequence contained an oligo-dT track that was present in the  
CC oligonucleotide that was used to prime the synthesis of first  
CC strand cDNA and therefore this may represent a bonafide poly A  
CC tail. The sequence tag present in the cDNA between the NotI site  
CC and the oligo-dT track served to identify it as a clone from the  
CC normalized anterior pituitary at estrus day 12 library cDNA library  
CC Preparation: RJ Woods, JA Green, RS Prather SI42 Animal Science  
CC Research Center, Department of Animal Science, University of  
CC Missouri-Columbia, 65211 Clone distribution: clones will be  
CC available through Research Genetics (www.resgen.com)  
CC Seq primer: M13 Forward  
CC POLYA=Yes.  
XX  
FH Key Location/Qualifiers  
FH source 1. .308  
FT /db\_xref="taxon:9823"  
FT /db\_xref="UNILIB:9699"  
FT /note="Vector: pT73D-Pac (Pharmacia) with a modified  
FT polynuker; Site 1: Not I; Site 2: EcoRI; The MI-P-NA is a  
FT normalized library comprised of anterior pituitary tissue  
FT at estrus days 0, 5, and 12. For a detailed description of  
FT the library from which this clone was derived, please  
FT visit our web site at <http://pigest.genome.iastate.edu/>.  
FT TAG LIB=MI-P-NA TAG\_TISSUE=anterior pituitary at estrus day  
FT 12 TAG SEQ=TCACAG"  
FT /organism="Sus scrofa"  
FT /strain="crossbreed"  
FT /clone="MI-P-NA-aeg-e-07-1-UM.abi"  
FT /clone\_lib="MI-P-NA"  
FT /lab\_host="DHI0B (Life Technologies)"  
FT  
XX Sequence 308 BP; 134 A; 51 C; 57 G; 66 T; 0 other;

Query Match 1.88; Score 35.6; DB 9; Length 308;  
Best Local Similarity 52.74; Pred. No. 3.9; Indels 0; Gaps 0;  
Matches 77; Conservative 0; Mismatches 69; Indels 0; Gaps 0;  
QY 1630 TTGTCATTCTGATTTCGATTTATATCTGTTATCGGTCTAAAGTCTAAATTTACCCA 1689  
Db 250 TTTTCTTTTCTGCTAGACAGATTAACATTTTCAATTTTGGCAGACACTTTTTT 1749  
QY 1690 TTTGATTTTCTGCTAGACAGATTAACATTTTCAATTTTGGCAGACACTTTTTT 1749  
Db 190 CCCAATTCCTCTTTTGGGGTTTTGTTTTTTTGAATTTTCCCGCCGTTTTCTT 131  
QY 1750 TTTTCTTTGAAATCTTTCTTCCCTCCAG 1775  
Db 130 TTTTCTTTGAAAGGTTTCTCCCAAG 105

RESULT 2  
ID AU212636/c standard; RNA; EST; 659 BP.  
XX AU212636  
AC AU212636;  
XX AU212636.1  
SV AU212636.1  
DT 17-JUL-2001 (Rel. 68, Created)  
DT 17-JUL-2001 (Rel. 68, Last updated, Version 1)  
XX  
XX Caenorhabditis elegans cDNA clone:yk787h01 : 3' end, single read.  
XX EST (expressed sequence tag).  
XX  
XX Caenorhabditis elegans  
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.

XX [1]  
RN 1-659  
RP Kohara Y.;  
RA  
RT Submitted (10-JUL-2001) to the EMBL/GenBank/DBJ databases.  
RL Yuji Kohara, National Institute of Genetics, Genome Biology Lab.; 1111  
RL Yata, Mishima, Shizuoka 411-8540, Japan (E-mail:ykohara@lab.nig.ac.jp,  
RL Tel:81-559-81-6854, Fax:81-559-81-6855)  
XX [2]  
RN Kohara Y., Shin-i T., Thierry-Mieg J., Thierry-Mieg D., Suzuki Y.,  
RA Sugano S.;  
RA "A complementary view of the C.elegans genome.";  
RT Unpublished.  
RL  
XX UNILIB; 9635; 9635.  
DR  
FH Key Location/Qualifiers  
FH source 1. .659  
FT /db\_xref="taxon:6239"  
FT /db\_xref="UNILIB:9635"  
FT /sequenced\_mol="cDNA to mRNA"  
FT /sex="Hermaphrodite"  
FT /organism="Caenorhabditis elegans"  
FT /clone="yk787h01"  
FT /clone\_lib="unpublished oligo-capped cDNA library"  
FT /dev\_stage="L4"  
FT /strain="N2"  
FT /tissue\_type="whole animal"  
XX  
SQ Sequence 659 BP; 160 A; 162 C; 130 G; 205 T; 2 other;  
Query Match 1.74; Score 35.2; DB 3; Length 659;  
Best Local Similarity 51.64; Pred. No. 4;  
Matches 79; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
QY 1578 GTATTCGTATAAATCTCTTGAATAATCTGAAATCAAGGTTAAATGTTTGTTCAT 1637  
Db 165 GTTTCATTAATAATACAAATTTGAATTTCTCTAATTAATCTTTATTCATTTCTCTAT 106  
QY 1638 TCTGATTTGTCATTTTATTTATCTGTTATCGGTCTAAAGTCTAAATTTACCATTTGATTT 1697  
Db 105 CCCGATTTTCTCTCCAGTTTGTGAACGCTTCCAGTATCTCAGTCACAGAGTTTCATT 46  
QY 1698 TTTGCTAGACAGATTAACATTTTAATTTTTCAAA 1730  
Db 45 TATTTGTTCCACTTTTAAATATTTATTNAGTAAA 13  
RESULT 3  
BF713200/c standard; RNA; EST; 195 BP.  
ID BF713200  
XX BF713200;  
XX BF713200.1  
SV BF713200.1  
XX  
DT 03-JAN-2001 (Rel. 66, Created)  
DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)  
XX  
XX MI-P-O2-ads-f-01-1-UM.sl MI-P-O2 Sus scrofa cDNA clone  
DE MI-P-O2-ads-f-01-1-UM 3', mRNA sequence.  
XX  
XX EST.  
XX  
XX Sus scrofa (pig)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
XX [1]  
RN 1-195



```

RX MEDLINE; 97044477.
RA Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL discovery";
RL Genome Res. 6(9):791-806(1996).
DR UNILIB; 7284; 7284.
XX
CC Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. cDNA library Preparation: RJ Woods, JA Green, RS Prather S142
CC Animal Science Research Center, Department of Animal Science,
CC University of Missouri-Columbia, 65211 Clone distribution: clones
CC will be available through Research Genetics (www.resgen.com) The
CC following repetitive elements were found in this cDNA sequence:
CC 63-162, >(TAAAA)n#simple_repeat 85-158, >POLY_A#simple_repeat
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
FH Key Location/Qualifiers
FH source
FH 1. .195
FH /db_xref="taxon:9823"
FH /db_xref="UNILIB:7284"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site 1: Not 1; Site 2: EcoRI; The MI-P-02
FH library is derived from ovary at estrus day 5. For a
FH detailed description of the library from which this clone
FH was derived, please visit our web site at
FH http://pigest.genome.iastate.edu/. TAG_SEQ=None found"
FH /organism="Sus scrofa"
FH /strain="crossbreed"
FH /clone="MI-P-02-ads-f-01-1-UM"
FH /clone_lib="MI-P-02"
FH /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 195 BP; 107 A; 14 C; 21 G; 53 T; 0 other;

Query Match 1.6%; Score 32.6; DB 9; Length 195;
Best Local Similarity 48.8%; Pred. No. 15;
Matches 89; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 1287 TTTCCTTTCTGTGCTGATTTTGGCCAGATCGATCTGCATTTATTTCTACTTTTCT 1346
DB 194 TTTCCTTTCTGTGCTGATTTTGGCCAGATCGATCTGCATTTATTTCTACTTTTCT 135
QY 1347 ATGTATTATATCTCTGATGAGTCACTAATAAGAGCAGTATTTTTTTTGTGACGTATCA 1406
DB 134 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 75
QY 1407 ATCGACTGATCTAATGTGAATAGTATCTCTTAAACCAAGCAGTCTATTTTGGCAG 1466
DB 74 CGCATTTTATTCAATAAATAACTTCAGTAACAGCAGCTGTAAAGAGTGAACCTGTTAAAA 15
QY 1467 AAA 1469
DB 14 AAA 12

RESULT 4
BI400626/c
ID BI400626 standard; RNA; EST; 465 BP.
XX
AC BI400626;
XX

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SV BI400626.1
XX
DT 15-AUG-2001 (Rel. 68, Created)
DT 15-AUG-2001 (Rel. 68, Last updated, Version 1)
XX
DE MI-P-AV1-hqf-f-07-0-UI.s1 MI-P-AV1 Sus scrofa cDNA clone
DE MI-P-AV1-hqf-f-07-0-UI 3', mRNA sequence.
XX
XX EST.
XX
OS Sus scrofa (pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
XX [1]
XX MEDLINE; 97044477.
XX Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL discovery";
RL Genome Res. 6(9):791-806(1996).
DR UNILIB; 7287; 7287.
XX
CC Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC normalized placenta library cDNA library Preparation: M.B. Soares
CC Lab, University of Iowa EST sequencing: M.B. Soares Lab, University
CC of Iowa Clone distribution: clones will be available through
CC Research Genetics (www.resgen.com) The following repetitive
CC elements were found in this cDNA sequence: 46-176.
CC >POLY_A#simple_repeat 405-452, >POLY_A#simple_repeat
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
FH Key Location/Qualifiers
FH source
FH 1. .465
FH /db_xref="taxon:9823"
FH /db_xref="UNILIB:7287"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site 1: Not 1; Site 2: EcoRI; The MI-P-AV1
FH library is normalized library derived from the MI-P-AV0
FH library, ultimately derived from placenta tissue. For a
FH detailed description of the library from which this clone
FH was derived, please visit our web site at
FH http://pigest.genome.iastate.edu/. The procedure used to
FH create this library has been previously described (Bonaldo
FH , Lennon and Soares, Genome Research 6: 791-806, 1996)
FH TAG_LIB=MI-P-AV1 TAG_TISSUE=placenta TAG_SEQ=ATTGG"
FH /organism="Sus scrofa"
FH /strain="crossbreed"
FH /clone="MI-P-AV1-hqf-f-07-0-UI"
FH /clone_lib="MI-P-AV1"
FH /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 465 BP; 255 A; 83 C; 74 G; 53 T; 0 other;

Query Match 1.6%; Score 32.2; DB 9; Length 465;
Best Local Similarity 54.7%; Pred. No. 15;
Matches 64; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1641 GATTTGTCATTTTATTATCTGTTATCGTCTAAAGTCTAATTTACCCATTTTTC 1700

```



FT first strand cDNA was synthesized from oligo dT-selected  
 FT mRNA by priming with dT-tailed vector. The dT-tailed vector  
 FT was adjusted to have about 60nt. The cDNA vector was  
 FT circularized with E. coli DNA ligase after digestion of  
 FT EcoRI which site is also included in vector. An RNA strand  
 FT converted to a DNA strand by Okayama-Berg method. The  
 FT obtained cDNA vectors were used for transformation of  
 FT competent cells E. coli Top10F' by electroporation method."  
 FT /sex="M"  
 FT /organism="Homo sapiens"  
 FT /clone="S5SNU484-13-H05"  
 FT /clone\_lib="S5SNU484"  
 FT /tissue\_type="Stomach"  
 FT /cell\_type="Epithelial"  
 FT /cell\_line="SNU-484"  
 FT /lab\_host="Top10F' "  
 FT  
 XX  
 XX

SQ Sequence 500 BP; 189 A; 103 C; 108 G; 100 T; 0 other;

Query Match 1.5%; Score 31.4; DB 2; Length 500;  
 Best Local Similarity 49.7%; Pred. No. 21;  
 Matches 80; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 1619 TTAATGATTTTGTTCATCTGATTTGTCATTTTATTATCTGTTAAAGTGC 1678

Db 347 TTTTGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAACCATATT 288

QY 1679 TAATTTACCATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGCGAG 1738

Db 287 CAATTTATGACATGTCAATTTATGACAGACAGAGATTTTTTTTTTCCCATGGAT 228

QY 1739 ACATTTTTTTTTTTTTTTTGAATCTTTTCCATCATCT 1779

Db 227 GAGATCCTTTTCAATCGCCATAACATGTGCCACACATCT 187

# RESULT 7

ID BF702953/c standard; RNA; EST; 556 BP.

AC BF702953;

SV BF702953.1

25-DEC-2000 (Rel. 66, Created)

25-DEC-2000 (Rel. 66, Last updated, Version 1)

XX MI-P-H1-abj-b-05-1-UM.s1 MI-P-H1 Sus scrofa cDNA clone

DE MI-P-H1-abj-b-05-1-UM 3', mRNA sequence.

XX EST.

XX

OS Sus scrofa (pig)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

XX [1]

RP 1-556

XX MEDLINE; 97044477.

RA Bonaldo M.F., Lennon G., Soares M.B.;

RT "Normalization and subtraction: two approaches to facilitate gene

discovery";

RL Genome Res. 6(9):791-806(1996).

XX

DR UNILB; 7279; 7279.

XX

CC Contact: Tuggle CK

CC Molecular Genetics Laboratory, Department of Animal Science

CC Iowa State University

CC 201 Kildes Hall, Ames, IA 50011-3150, USA

CC Tel: 5152944252

CC Fax: 5152942401

CC Email: cktuggle@iastate.edu

CC The sequence contained an oligo-dT track that was present in the  
 CC oligonucleotide that was used to prime the synthesis of first  
 CC strand cDNA and therefore this may represent a bonafide poly A  
 CC tail. The sequence tag present in the cDNA between the NotI site  
 CC and the oligo-dT track served to verify it as a clone from the  
 CC non-normalized hypothalamus at estrus day 0 library cDNA Library  
 CC Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science  
 CC Research Center, Department of Animal Science, University of  
 CC Missouri-Columbia, 65211 Clone Distribution: clones will be  
 CC available through Research Genetics (www.resgen.com) The following  
 CC repetitive elements were found in this cDNA sequence: 69-193,  
 CC >POLY\_A#Simple\_repeat 264-316, >POLY\_A#Simple\_repeat 525-548,  
 CC >AT\_rich#Low\_complexity  
 CC Seq primer: M13 Forward  
 CC POLYA=Yes.

XX Key Location/Qualifiers

FT source 1..556

FT /db\_xref="taxon:9823"

FT /db\_xref="UNILB:7279"

FT /note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker: Site 1: Not I; Site 2: EcoRI; The MI-P-H1

library is derived from hypothalamus at estrus day 0. For

a detailed description of the library from which this

clone was derived, please visit our web site at

http://pigest.genome.iastate.edu/. TAG LIB-MI-P-H1

TAG TISSUE=hypothalamus at estrus day 0 TAG\_SEQ=TAGATG"

/organism="Sus scrofa"

/strain="crossbreed"

/clone="MI-P-H1-abj-b-05-1-UM"

/clone\_lib="MI-P-H1"

/lab\_host="DH10B (Life Technologies)"

XX

SQ Sequence 556 BP; 268 A; 117 C; 102 G; 69 T; 0 other;

Query Match 1.5%; Score 31.4; DB 9; Length 556;

Best Local Similarity 51.8%; Pred. No. 20;

Matches 71; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1650 TTTTATATCTGTTATCGTCTAAAGTCTAATTTTACCATTGATTTCTCTGCTAGACA 1709

Db 189 TTTTATTTTGGGAACCCCTTTTTCATTTTCCCCCCCAATTTTTTGGTTT 130

QY 1710 GATAACTTTTAAATTTTCAAAATTTGCAGACACTTTTTTTTTTTTCAAAATCTTTC 1769

Db 129 TTTAAATTTGGAATTTGGCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTT 70

QY 1770 TTCAGATCTGTTGCC 1786

Db 69 TCCCAGGGTTTTTTTCC 53

# RESULT 8

HSN010501

ID HSN010501 standard; RNA; EST; 136 BP.

XX AC AL045651;

XX SV AL045651.1

XX

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX

DE Homo sapiens mRNA; EST DKFZp434P095\_s1 (from clone DKFZp434P095)

XX

XX EST; expressed sequence tag.

XX

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX

RN [1]

```

RP 1-136
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferapitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC r1 sequence also available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH source 1. .136
FH /db_xref="taxon:9606"
FH /organism="Homo sapiens"
FH /clone_lib="DKFZP434P095"
FH /DH10B; sites NotI + SalI
FH /dev stage="adult"
FH /tissue_type="testis"
XX
SQ Sequence 136 BP; 8 A; 4 C; 4 G; 119 T; 1 other;

Query Match 1.5%; Score 31.2; DB 2; Length 136;
Best Local Similarity 53.2%; Pred. No. 28;
Matches 66; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 1639 CTGATTGTCATTTATCTGTTATCGGTCCTAAAGTCTAAATTTACCCATTTGATTTT 1698
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8 CTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 67

Qy 1699 TCTGCTAGACAGATACTTTAAATTTTCAAAATTTGCAGACACTTTTTTTTTTTT 1758
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 127

Qy 1759 AAAA 1762
|||
Db 128 AAAA 131

RESULT 9
BF712847/c standard; RNA; EST; 374 BP.
XX
AC BF712847;
XX
SV BF712847.1
XX
03-JAN-2001 (Rel. 66, Created)
DT
DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX
MI-P-Ol-ado-e-09-1-UM.s1 MI-P-Ol Sus scrofa cDNA clone
DE
DE MI-P-Ol-ado-e-09-1-UM 3', mRNA sequence.
XX
KW EST.
XX
XX Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
XX [1]
RP 1-1374
RX MEDLINE; 97044477.
RA Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RT discovery";
RL Genome Res. 6(9):791-806(1996).
XX
XX UNILIB; 7283; 7283.
DR
XX

```

```

CC Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142
CC Animal Science Research Center, Department of Animal Science,
CC University of Missouri-Columbia, 65211 Clone distribution: clones
CC will be available through Research Genetics (www.resgen.com) The
CC following repetitive elements were found in this cDNA sequence:
CC 39-154, >POLY_A#Simple repeat 254-359, >POLY_A#Simple_repeat
CC POLY_A=Yes.
XX
FH Key Location/Qualifiers
FH source 1. .374
FH /db_xref="taxon:9823"
FH /db_xref="UNILIB:7283"
FH /note="Vector: p773D-pac (Pharmacia) with a modified
FH polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-Ol
FH library is derived from ovary at estrus day 0. For a
FH detailed description of the library from which this clone
FH was derived, please visit our web site at
FH http://pigest.genome.iastate.edu/. TAG_SEQ=None found"
FH /organism="Sus scrofa"
FH /strain="crossbred"
FH /clone_lib="MI-P-Ol-ado-e-09-1-UM"
FH /clone_lib="MI-P-Ol"
FH /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 374 BP; 224 A; 29 C; 72 G; 49 T; 0 other;

Query Match 1.5%; Score 31.2; DB 9; Length 374;
Best Local Similarity 52.3%; Pred. No. 24;
Matches 69; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 1626 TTTTTCCTCATCTGATTTGTCATTTTATATCTGTAATGCTAAAGTGTAAATTTA 1685
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 223 TTTTTCCTCATCTGATTTGTCATTTTATATCTGTAATGCTAAAGTGTAAATTTA 164
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1686 CCCATTTGATTTTTCGCTAGACAGATACTTTTAAATTTTCAAAATTTGCAGACACTTT 1745
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 163 TTTTTCCTCATCTGATTTGTCATTTTATATCTGTAATGCTAAAGTGTAAATTTA 104
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1746 TTTTTCCTCATCTGATTTGTCATTTTATATCTGTAATGCTAAAGTGTAAATTTA 1757
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 103 TTTTTCCTCATCTGATTTGTCATTTTATATCTGTAATGCTAAAGTGTAAATTTA 92

RESULT 10
HSM002682/c standard; RNA; EST; 472 BP.
XX
AC AL038339;
XX
SV AL038339.1
XX
12-MAR-1999 (Rel. 59, Created)
DT
DT 25-SEP-1999 (Rel. 61, Last updated, Version 3)
XX
XX Homo sapiens mRNA; EST DKFZp566K192_r1 (from clone DKFZp566K192)
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

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DE MI-P-H1-abm-b-03-1-UM 3', mRNA sequence.
XX EST.
XX
XX Sus scrofa (pig)
OS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
XX [1]
RN 1-502
RP MEDLINE; 97044477.
RA Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subraction: two approaches to facilitate gene
RL discovery";
RL Genome Res. 6(9):791-806(1996).
XX
XX UNILIB; 7279; 7279.
XX
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized hypothalamus at estrus day 0 library cDNA Library
CC Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science
CC Research Center, Department of Animal Science, University of
CC Missouri-Columbia, 65211 Clone distribution: clones will be
CC available through Research Genetics (www.resgen.com) The following
CC repetitive elements were found in this cDNA sequence: 161-198,
CC >POLY(A)Simple repeat 199-221, >GC-rich#Low_complexity 245-269,
CC >GC-rich#Low_complexity
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
XX Key Location/Qualifiers
FH source 1..502
FH /db_xref="taxon:9823"
FT /db_xref="UNILIB:7279"
FT /notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
FT polylinker; Site_1: Not I; Site_2: ScaRI; The MI-P-H1
FT library is derived from hypothalamus at estrus day 0. For
FT a detailed description of the library from which this
FT clone was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. TAG_LIB=MI-P-H1
FT TAG_TISSUE=hypothalamus at estrus day 0 TAG_SEQ=TAGATG"
FT /organism="Sus scrofa"
FT /strains="crossbred"
FT /clone="MI-P-H1-abm-b-03-1-UM"
FT /clone_lib="MI-P-H1"
FT /lab_host="DH10B (Life Technologies)"
XX
XX Sequence 502 BP; 175 A; 130 C; 99 G; 98 T; 0 other;

Query Match 1.5%; Score 30.6; DB 9; Length 502;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 51; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 1678 CTAATTACCACTTGTATTTCTGCTAGACAGATACCTTTAATTTTCAAAATGGCA 1737
DB 187 CTTTCTTTTATATTTTGTGTTTGGGGGCCAAACTTTTGTAAAGGGGCC 128
QY 1738 GACACTTTTTTTTTTTTTTGAATA 1762
DB 127 CCCCGTTTTTTTTTTGGGGGAAA 103

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RESULT 13
BQ236337/c standard; RNA; EST; 321 BP.
ID BQ236337
XX
XX AC BQ236337;
XX SV BQ236337.1
XX
XX 04-MAY-2002 (Rel. 71, Created)
DT 04-MAY-2002 (Rel. 71, Last updated, Version 1)
XX
DE TAE05035A09F TAE05 Triticum aestivum cDNA clone TAE05035A09F, mRNA
DE sequence.
DE XX XX
DE KW EST.
XX
XX Triticum aestivum (bread wheat)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
XX
XX [1]
RN 1-321
RP Cloutier S.;
RT "Wheat functional genomics - Glenlea developing seeds cDNA libraries";
RL Unpublished.
XX
XX UNILIB; 10545; 10545.
XX
XX Contact: Dr. Sylvie Cloutier
CC Cereal Research Centre, Agriculture and Agri-food Canada
CC 195 Daffoe Rd, Winnipeg, MB, Canada R3T 2M9
CC Tel: (204) 983-2340
CC Fax: (204) 983-4604
CC Email: scloutier@em.agr.ca
CC was cloned directionally, not all sequences generated with reverse
CC primer were from the 5' end (same with forward primer and 3' end).
CC Average insert size is >2.0 kb
CC Plate: 035 row: A column: 09
CC Seq primer: M13 Forward.
XX
XX Key Location/Qualifiers
FH source 1..321
FH /db_xref="taxon:4565"
FT /db_xref="UNILIB:10545"
FT /notes="Vector: Lambda ZapII; mass excised in plasmid vector
FT pSPORT-P (Invitrogen Technologies); Site_1: NotI; Site_2:
FT MluI; mRNA obtained from wheat seeds of Cultivar Glenlea 5
FT days post-anthesis"
FT /organism="Triticum aestivum"
FT /cultivar="Glenlea"
FT /clone="TAE05035A09F"
FT /clone_lib="TAE05"
FT /tissue_type="developing seeds"
FT /dev_stage="5 days after anthesis"
FT /lab_host="E. coli DH10B"
XX
XX Sequence 321 BP; 170 A; 64 C; 35 G; 52 T; 0 other;

Query Match 1.5%; Score 30.2; DB 6; Length 321;
Best Local Similarity 51.1%; Pred. No. 37;
Matches 71; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1619 TTAATGATTTTTTGTTCATTCGATTTGTCAATTTATATCTGTTATCGGTCATAAGTGC 1678
DB 251 TTTTGTGTTTGGGGGCCCTTTAAATTTCCCTTTAAAGGGGGGTTTGTGTTGT 192
QY 1679 TAAATTTACCCATTTGATTTTTTCTGCTAGACAGATAACTTTTAAATTTTCAATTTGCGAG 1738
DB 191 TGTTTTTAAATAAAAAAATTTTTTTTTTTTCTGTTTATTTTTTTTTCG 132

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SQ Sequence 273 BP; 128 A; 44 C; 34 G; 65 T; 2 other;
  Query Match      1.5%; Score 30; DB 2; Length 273;
  Best Local Similarity 52.9%; Pred. No. 41;
  Matches 63; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 1282 GCATCTTGGCTTCTGTCCTGATTTTCCAGATGGAATCGCAATTAATTTGTAATT 1341
  |||||
Db 257 GGATCGATTAGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 198
  |||||
QY 1342 TTTCTATGATTATATCCTCTAGAGTCACTAATAAGGAGTATTTTCTGTCAGC 1400
  |||||
Db 197 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 139
  |||||
  RESULT 16
  BF711870/c
  ID BF711870 standard; RNA; EST; 300 BP.
  XX AC BF711870;
  SV BF711870.1
  XX 03-JAN-2001 (Rel. 66, Created)
  DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
  XX MI-P-O3-abg-a-07-1-UM.s1 MI-P-O3 Sus scrofa cDNA clone
  DE MI-P-O3-abg-a-07-1-UM 3', mRNA sequence.
  XX EST.
  XX Sus scrofa (pig)
  OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
  OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
  XX [1]
  RN 1-300
  RP MEDLINE; 97044477.
  RA Bonaldo M.F., Lennon G., Soares M.B.;
  RT "Normalization and subtraction: two approaches to facilitate gene
  RL discovery";
  RL Genome Res. 6(9):791-806(1996).
  XX
  XX UNILIB; 7285; 7285.
  XX Contact: Tuggle CK
  CC Molecular Genetics Laboratory, Department of Animal Science
  CC Iowa State University
  CC 201 Kildee Hall, Ames, IA 50011-3150, USA
  CC Tel: 5152944252
  CC Fax: 5152942401
  CC Email: ktuggle@iastate.edu
  CC The sequence contained an oligo-dT track that was present in the
  CC oligonucleotide that was used to prime the synthesis of first
  CC strand cDNA and therefore this may represent a bonafide poly A
  CC tail. cDNA library preparation: RJ Woods, JA Green, RS Prather S142
  CC Animal Science Research Center, Department of Animal Science,
  CC University of Missouri-Columbia, 65211 Clone distribution: clones
  CC will be available through Research Genetics (www.resgen.com) The
  CC following repetitive elements were found in this cDNA sequence:
  CC 65-138, >POLY_ASimple repeat 169-269, >GC_richLow_complexity
  CC Seq primer: M13 Forward
  CC POLYA=Yes.
  XX
  XX Key Location/Qualifiers
  FH source
  FT 1. .300
  FT /db_xref="taxon:9823"
  FT /db_xref="UNILIB:7285"
  FT /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
  FT polylinker; Site 1: Not 1; Site 2: EcoRI; The MI-P-O3
  FT library is derived from ovary at estrus day 12. For a
  FT detailed description of the library from which this clone
  FT
```

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FT was derived, please visit our web site at
FT http://piglet.genome.fastate.edu/. TAG_SEQ=None found"
FT /organism="Sus scrofa"
FT /strain="Croesebreed"
FT /clone="MI-P-O3-abg-a-07-1-UM"
FT /lab_host="MI-P-O3"
FT /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 300 BP; 100 A; 98 C; 59 G; 43 T; 0 other;
  Query Match      1.5%; Score 29.8; DB 9; Length 300;
  Best Local Similarity 51.1%; Pred. No. 44;
  Matches 70; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 1257 TCGTCCCGTGGGGGGTGTGATGTTGCATCTTTGCCCTTCTTGCTGTTGATTTTGGCCA 1316
  |||||
Db 174 TCGGCTGTGTGTTGTTGTTTGGGGCCGCTGCTTTTCTTTTGTGGGCC 115
  |||||
QY 1317 GATGGATCTGCATTTATTTCTACTTTTCTTATGTTATTAATCTGTAGAAGTCACCTAAT 1376
  |||||
Db 114 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 55
  |||||
QY 1377 AAGGAGTATTTTCTTTT 1393
  |||||
Db 54 AGCTGTGACTTTTATT 38
  |||||
  RESULT 17
  HSM010205
  ID HSM010205 standard; RNA; EST; 127 BP.
  XX AC AL045355;
  XX AL045355.1
  XX 12-MAR-1999 (Rel. 59, Created)
  DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
  XX Homo sapiens mRNA; EST DKF2p434B085.s1 (from clone DKF2p434B085)
  DE EST; expressed sequence tag.
  XX
  XX Homo sapiens (human)
  OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
  OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
  XX [1]
  RN 1-127
  RP Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
  RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
  RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
  XX
  CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
  CC sequencing consortium of the German Genome Project
  CC ri sequence also available
  CC This clone is available at the RZPD in Berlin
  CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
  CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
  XX
  XX Key Location/Qualifiers
  FH source
  FT 1. .127
  FT /db_xref="taxon:9606"
  FT /organism="Homo sapiens"
  FT /clone="DKF2p434B085"
  FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
  FT DH10B; sites NotI + SalI"
  FT /dev_stage="adult"
  FT /tissue_type="testis"
  XX
  XX Sequence 127 BP; 2 A; 5 C; 2 G; 116 T; 2 other;
  SQ
```



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Query Match      1.5%; Score 29.6; DB 2; Length 127;
Best Local Similarity 52.5%; Pred. No. 56;
Matches 62; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1643 TTGTGCTATTTTATCTGTTATCTGCTCTAAAGTGTAAATTTACCCATTTGATTTTCTG 1702
DB 10 TTTTNTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 69

QY 1703 CTAGACAGATAACTTTTAAATTTTCAAAATTTGCACACACTTTTTTTTTTTTTTTTGGAA 1760
DB 70 TTTTNTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 127

RESULT 18
HSM003359/c
ID HSM003359 standard; RNA; EST; 147 BP.
AC AL038883;
SV AL038883.1
XX
XX
XX 12-MAR-1999 (Rel. 59, Created)
XX 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp566E0247_r1 (from clone DKFZp566E0247)
XX
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
XX
XX Ottenwaelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by MediGenomix within the cDNA
XX sequencing consortium of the German Genome Project
XX No sl sequence available
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
FH source 1..147
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp566E0247"
FT /clone_lib="566 (synonym: hfk2). Vector pAMP1; host
FT XI-2blue; sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="kidney"
XX
XX Sequence 147 BP; 94 A; 14 C; 12 G; 27 T; 0 other;

Query Match      1.4%; Score 29.4; DB 2; Length 147;
Best Local Similarity 54.1%; Pred. No. 59;
Matches 60; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1293 TTTCTGCTGCTGATTTTCCAGATGGATCGCATTTATTTTGTACTTTTCTATCTAT 1352
DB 145 TTTTNTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 86

QY 1353 TATAATCCTGTAGAGTCACATAAAGGAGTATTTTTTTTGTGACGCTTA 1403
DB 85 TTTTNTTAAAGAGAGGTCACATCAATAGTCTTTTATTGCAATCAATTAA 35

RESULT 19
BF711427/c
ID BF711427 standard; RNA; EST; 150 BP.
AC BF711427;
SV BF711427.1
XX
XX 03-JAN-2001 (Rel. 66, Created)
XX 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX
DE MI-P-A2-acp-e-06-1-UM.sl MI-P-A2 Sus scrofa cDNA clone
XX MI-P-A2-acp-e-06-1-UM 3', mRNA sequence.
XX
XX EST.
XX
XX Sus scrofa (pig)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
XX
XX 1-150
XX MEDLINE; 97044477.
XX Ronaldo M.F., Lennon G., Soares M.B.;
XX "Normalization and subtraction: two approaches to facilitate gene
XX discovery";
XX Genome Res. 6(9):791-806(1996).
XX
XX UNILIB; 7272; 7272.
XX
XX Contact: Tuggle CK
XX Molecular Genetics Laboratory, Department of Animal Science
XX Iowa State University
XX 201 Kildee Hall, Ames, IA 50011-3150, USA
XX Tel: 5152944252
XX Fax: 5152942401
XX Email: cktuggle@iastate.edu
XX
XX The sequence contained an oligo-dT track that was present in the
XX oligonucleotide that was used to prime the synthesis of first
XX strand cDNA and therefore this may represent a bonafide poly A
XX tail. The sequence tag present in the cDNA between the NotI site
XX and the oligo-dT track served to verify it as a clone from the
XX non-normalized anterior pituitary at estrus day 5 library cDNA
XX Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal
XX Science Research Center, Department of Animal Science, University
XX of Missouri-Columbia, 65211 Clone distribution: clones will be
XX available through Research Genetics (www.resgen.com) The following
XX repetitive elements were found in this cDNA sequence: 27-80,
XX >POLY_A#Simple_repeat
XX Seq primer: M13 Forward
XX POLYA=Yes.
XX
XX Key Location/Qualifiers
FH source 1..150
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7272"
FT /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-A2
FT library is derived from anterior pituitary at estrus day 5.
FT For a detailed description of the library from which this
FT clone was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. TAG LIB=MI-P-A2
FT TAG_TISSUE=anterior pituitary at estrus day 5
FT TAG_SEQ="CCGGT"
FT /organism="Sus scrofa"
FT /strain="crossbreed"
FT /clone="MI-P-A2-acp-e-06-1-UM"
FT /clone_lib="MI-P-A2"
FT /lab_host="DH10B (Life Technologies)"
XX
XX Sequence 150 BP; 71 A; 4 C; 20 G; 55 T; 0 other;

Query Match      1.4%; Score 29.4; DB 9; Length 150;

```

```
Best Local Similarity 66.7%; Pred. No. 59;
Matches 42; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1705 AGACAGATAACTTTAAATTTTCAAAATTTGGCAGACACTTTTTTTTTTTTTCGAAATC 1764
Db 90 AGTGAATAATTTCCCTTTTGTGTTTGTTCCTTTTCCATTTTATTTTATTTTAAAT 31
QY 1765 TTT 1767
Db 30 TTT 28

RESULT 20
BF712867/c standard; RNA; EST; 414 BP.
XX BF712867;
AC BF712867;
XX BF712867;
SV BF712867.1
XX 03-JAN-2001 (Rel. 66, Created)
DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX MI-P-Ol-ado-h-08-1-UM.s1 MI-P-Ol Sus scrofa cDNA clone
DE MI-P-Ol-ado-h-08-1-UM 3', mRNA sequence.
XX KW EST.
XX Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
RN 1-414
RP MEDLINE; 97044477.
RX Bonaldo M.F., Lennon G., Soares M.B.;
RA "Normalization and subtraction: two approaches to facilitate gene
RT discovery";
RL Genome Res. 6(9):791-806(1996).
XX UNILIB; 7283; 7283.
DR Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: ktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. cDNA library preparation: RJ Woods, JA Green, RS Prather S142
CC Animal Science Research Center, Department of Animal Science,
CC University of Missouri-Columbia, 65211 Clone distribution: clones
CC will be available through Research Genetics (www.resgen.com) The
CC following repetitive elements were found in this cDNA sequence:
CC 209-313 >POLY.A#Simple_repeat 366-405, >AT-rich#Low_complexity
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX Key Location/Qualifiers
FH 1. .414
FH /db_xref="taxon:9823"
FT /note="vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not 1; Site 2: EcoRI; The MI-P-Ol
FT library is derived from ovary at estrus day 0. For a
FT detailed description of the library from which this clone
FT was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. TAG_SEQ=None found"
FT /organism="Sus scrofa"
```

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FT /strain="crossbreed"
FT /clone="MI-P-Ol-ado-h-08-1-UM"
FT /clone_lib="MI-P-Ol"
FT /lab_host="DH10B (Life Technologies)"
XX Sequence 414 BP; 189 A; 46 C; 83 G; 96 T; 0 other;
QY Query Match 1.4%; Score 29.4; DB 9; Length 414;
Best Local Similarity 47.1%; Pred. No. 49;
Matches 90; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 1564 TTTTGTCATTTAGAGTATTCGTATAAAATCTTTGAAAACTGAAATCAAAGGTTAAT 1623
Db 399 TTTTATTTTACCAAAATTTTTCGAATTTTTTTTCCCTTCCAAAAAATTTTCG 340
QY 1624 GATTTTTTGTTCATTCGTGATTTGCTATTTATTTATCTGTTATCGTAAAGTCTAAT 1683
Db 339 GGTTTTCCCGGTTTCCCTTAAAAATTTTTTTCCTTTTTTTTTTAAAGTTTTCCT 280
QY 1684 TACCATTTGATTTTCTGCTAGACAGATAACTTTTAAATTTTTCAAATTTGGCAGACACT 1743
Db 279 TCCCTTTTGGGGTATTTTTCGGTTTCAAAATCCCTTTACCCAATACCTTTTTTT 220
QY 1744 TTTTTTTTTTTT 1754
Db 219 TTGTTTTTTTTT 209

RESULT 21
BF704037/c standard; RNA; EST; 417 BP.
XX BF704037;
AC BF704037;
XX BF704037.1
SV BF704037.1
XX 26-DEC-2000 (Rel. 66, Created)
DT 26-DEC-2000 (Rel. 66, Last updated, Version 1)
XX MI-P-A3-abw-c-09-1-UM.s1 MI-P-A3 Sus scrofa cDNA clone
DE MI-P-A3-abw-c-09-1-UM 3', mRNA sequence.
XX KW EST.
XX Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
RN 1-417
RP MEDLINE; 97044477.
RX Bonaldo M.F., Lennon G., Soares M.B.;
RA "Normalization and subtraction: two approaches to facilitate gene
RT discovery";
RL Genome Res. 6(9):791-806(1996).
XX UNILIB; 7273; 7273.
DR Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: ktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized anterior pituitary at estrus day 12 library cDNA
CC Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal
CC Science Research Center, Department of Animal Science, University
```

CC of Missouri-Columbia, 65211 Clone distribution: clones will be  
 CC available through Research Genetics (www.resgen.com) The following  
 CC repetitive elements were found in this cDNA sequence: 1-29,  
 CC >AT rich#Low complexity 56-193, >POLY\_A#Simple\_repeat  
 CC Seq primer: M13 Forward  
 CC POLVA=Yes.

XX Key Location/Qualifiers  
 FH source 1. .417  
 FT /db\_xref="taxon:9823"  
 FT /db\_xref="UNILIB:7273"  
 FT /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 FT polylinker; Site 1: Not 1; Site 2: EcoRI; The MI-P-A3  
 FT library is derived from anterior pituitary at estrus day  
 FT 12. For a detailed description of the library from which  
 FT this clone was derived, please visit our web site at  
 FT http://pigest.genome.iastate.edu/. TAG\_LIB=MI-P-A3  
 FT TAG\_TISSUE=anterior pituitary at estrus day 12  
 FT TAG\_SEQ=RGACAG"  
 FT /organism="Sus scrofa"  
 FT /strain="crossbreed"  
 FT /clone="MI-P-A3-abw-c-09-1-UM"  
 FT /clone\_lib="MI-P-A3"  
 FT /lab\_host="DH10B (Life Technologies)"  
 XX Sequence 417 BP; 219 A; 65 C; 70 G; 61 T; 2 other;

Query Match 1.4%; Score 29.4; DB 9; Length 417;  
 Best Local Similarity 66.7%; Pred. No. 49; Indels 0; Gaps 0;  
 Matches 42; Conservative 0; Mismatches 21;

QY 1695 TTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTTTTTTT 1754  
 |||||  
 DB 242 TTTTGGCTTTGGAAAAAAATTTTTCCTTCCCTTCCAGAAAAATTTTTTTT 183

QY 1755 TTT 1757  
 |||||  
 DB 182 TTT 180

RESULT 22  
 HS0001232/c  
 ID HSM001232 standard; RNA; EST; 144 BP.  
 XX AC AL036913;  
 XX SV AL036913.1  
 XX 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 DE Homo sapiens mRNA; EST DKFZp564B1164\_x1 (from clone DKFZp564B1164)  
 XX EST; expressed sequence tag.

XX Homo sapiens (human)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 XX [1]  
 RN Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;  
 RA 1-144  
 RP Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RT MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
 RL  
 CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA  
 CC sequencing consortium of the German Genome Project  
 CC No sl sequence available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers  
 FH source 1. .144  
 FT /db\_xref="taxon:9606"  
 FT /organism="Homo sapiens"  
 FT /clone="DKFZp564B1164"  
 FT /clone\_lib="564 (synonym: hEhr2). Vector pAMP1; host  
 FT X1-2blue; sites NotI + SalI"  
 FT /dev stage="fetal"  
 FT /tissue\_type="brain"  
 XX Sequence 144 BP; 119 A; 8 C; 4 G; 5 T; 8 other;

Query Match 1.4%; Score 29.2; DB 2; Length 144;  
 Best Local Similarity 49.6%; Pred. No. 64;  
 Matches 64; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1605 CTGAATCAAAAGGTTAATGATTTTGTTCATCTCGATTGTCATTTATATCTGTTA 1664  
 |||||  
 DB 137 CNGNTNNNNAANAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 78

QY 1665 TCGGCTAAAGTCTAAATTTACCATTTTCTGCTAGACAGATACTTTTAATT 1724  
 |||||  
 DB 77 TTT 18

QY 1725 TTCAAATTT 1733  
 |||||  
 DB 17 TTTTITTT 9

RESULT 23  
 BF713586/c  
 ID BF713586 standard; RNA; EST; 206 BP.  
 XX AC BF713586;  
 XX SV BF713586.1  
 XX 03-JAN-2001 (Rel. 66, Created)  
 DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)  
 XX MI-P-O2-adx-d-09-1-UM.sl MI-P-O2 Sus scrofa cDNA clone  
 DE MI-P-O2-adx-d-09-1-UM 3', mRNA sequence.  
 XX EST.

XX Sus scrofa (pig)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 XX [1]  
 RN MEDLINE; 97044477.  
 RA Ronaldo M.F., Lennon G., Soares M.B.;  
 RT "Normalization and subtraction: two approaches to facilitate gene  
 RT discovery";  
 RL Genome Res. 6(9):791-806(1996).  
 XX UNILIB; 7284; 7284.  
 XX Contact: Tuggle CK  
 CC Molecular Genetics Laboratory, Department of Animal Science  
 CC Iowa State University  
 CC 201 Kildee Hall, Ames, IA 50011-3150, USA  
 CC Tel: 5152944252  
 CC Fax: 5152942401  
 CC Email: cktuggle@iastate.edu  
 CC The sequence contained an oligo-dT track that was present in the  
 CC oligonucleotide that was used to prime the synthesis of first  
 CC strand cDNA and therefore this may represent a bonafide poly A  
 CC tail. cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142  
 CC Animal Science Research Center, Department of Animal Science,





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XX SQ Sequence 445 BP; 218 A; 84 C; 106 G; 37 T; 0 other;
Query Match 1.4%; Score 29.2; DB 9; Length 445;
Best Local Similarity 53.5%; Pred. No. 53;
Matches 61; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

XX BF711499 standard; RNA; EST; 445 BP.
AC BF711499;
SV BF711499.1
XX 03-JAN-2001 (Rel. 66, Created)
DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX MI-P-A2-acq-a-12-1-UM.s1 MI-P-A2 Sus scrofa cDNA clone
DE MI-P-A2-acq-a-12-1-UM 3', mRNA sequence.
XX EST.
XX Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
RN 1-445
RX MEDLINE; 97044477.
RA Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
discovery";
RL Genome Res. 6(9):791-806(1996).
XX UNILIB; 7272; 7272.
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized anterior pituitary at estrus day 5 library cDNA
CC Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal
CC Science Research Center, Department of Animal Science, University
CC of Missouri-Columbia, 65211 Clone distribution: clones will be
CC available through Research Genetics (www.resgen.com) The following
CC repetitive elements were found in this cDNA sequence: 19-154,
CC >POLY A#simple repeat 234-288, >POLY A#simple_repeat 295-319,
CC >GC_richLow_complexity
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX Key Location/Qualifiers
FH source 1. 445
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7272"
FT /note="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-A2
FT library is derived from anterior pituitary at estrus day 5.
FT For a detailed description of the library from which this
FT clone was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. TAG LIB=MI-P-A2
FT TAG TISSUE=anterior pituitary at estrus day 5
FT TAG_SEQ=TCGCGT"
FT /organism="Sus scrofa"
FT /strain="crossbreed"
FT /clone="MI-P-A2-acq-a-12-1-UM"
FT /clone_lib="MI-P-A2"
FT /lab_host="DH10B (Life Technologies)"

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XX SQ Sequence 445 BP; 218 A; 84 C; 106 G; 37 T; 0 other;
Query Match 1.4%; Score 29.2; DB 9; Length 445;
Best Local Similarity 53.5%; Pred. No. 53;
Matches 61; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

XX BF711499 standard; RNA; EST; 311 BP.
AC BF702714;
XX BF702714.1
SV BF702714.1
XX 25-DEC-2000 (Rel. 66, Created)
DT 25-DEC-2000 (Rel. 66, Last updated, Version 1)
XX MI-P-E3-aam-f-04-1-UM.s1 MI-P-E3 Sus scrofa cDNA clone
DE MI-P-E3-aam-f-04-1-UM 3', mRNA sequence.
XX EST.
XX Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
RN 1-311
RX MEDLINE; 97044477.
RA Bonaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
discovery";
RL Genome Res. 6(9):791-806(1996).
XX UNILIB; 7275; 7275.
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142
CC Animal Science Research Center, Department of Animal Science,
CC University of Missouri-Columbia, 65211 Clone distribution: clones
CC will be available through Research Genetics (www.resgen.com) The
CC following repetitive elements were found in this cDNA sequence:
CC 17-138, >POLY A#simple repeat 266-294, >GC_richLow_complexity
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX Key Location/Qualifiers
FH source 1. 311
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7275"
FT /note="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-E3
FT library is derived from fetus at gestational day 45. For a

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DR UNILIB; 7286; 7286.
XX
CC Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized placenta library cDNA Library Preparation: M.B.
CC Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
CC University of Iowa Clone distribution: clones will be available
CC through Research Genetics (www.resgen.com)
CC Seq primer: M13 Forward
CC POLYA=Yes.
FH
XX
FH Key Location/Qualifiers
FH
FT source
FT 1. 197
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7286"
FT /notes="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-AYO
FT library is derived from placenta. For a detailed
FT description of the library from which this clone was
FT derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. The procedure used to
FT create this library has been previously described (Bonaldo
FT , Lennon and Soares, Genome Research 6:791-806, 1996)
FT TAG_LIB=MI-P-AYO TAG_TISSUE=placenta TAG_SEQ=ATTGG"
FT /organism="Sus scrofa"
FT /clone="MI-P-AYO-neu-h-08-0-UI"
FT /clone_lib="MI-P-AYO"
FT /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 197 BP; 59 A; 58 C; 42 G; 38 T; 0 other;

Query Match 1.4%; Score 28.8; DB 9; Length 197;
Best Local Similarity 56.2%; Pred. No. 72;
Matches 54; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1853 GTGTGGAGGAGCTGAGAGTCTTGTAGTCTGCTCAGGTCGGGCGCATCTTGTGTTT 1912
Db 106 GGGTGGTTGGAAAAAACCCTGAGGCTTGTGGGGGGTGAGGTTTTTTTGGCC 47
QY 1913 GCATCTCTTTTAAATTTACACCTTTTCTTAAGAA 1948
Db 46 GGCCCCCTTTAAATTTTGTGCAAAAAA 11

RESULT 35
BF709877/c standard; RNA; EST; 313 BP.
XX
AC BF709877;
XX
SV BF709877.1
XX
DT 03-JAN-2001 (Rel. 66, Created)
DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX
DE MI-P-Ayi-npy-e-11-0-UI.s1 MI-P-Ayi Sus scrofa cDNA clone
DE MI-P-Ayi-npy-e-11-0-UI 3', mRNA sequence.
XX
KM EST.
XX
XX Sus scrofa (pig)
XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC

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OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
RN [1]
RX 1-313
RP MEDLINE; 97044477.
RA Bonaldo M.F.; Lennon G.; Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL discovery";
RL Genome Res. 6(9):791-806(1996).
XX
DR UNILIB; 7287; 7287.
XX
CC Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized placenta library cDNA Library Preparation: M.B. Soares
CC Lab, University of Iowa EST sequencing: M.B. Soares Lab, University
CC of Iowa Clone distribution: clones will be available through
CC Research Genetics (www.resgen.com) The following repetitive
CC elements were found in this cDNA sequence: 36-67,
CC >AT-rich#Low_complexity
CC Seq primer: M13 Forward
CC POLYA=Yes.
FH
XX
FH Key Location/Qualifiers
FH
FT source
FT 1. 313
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7287"
FT /notes="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-Ayi
FT library is normalized library derived from the MI-P-AYO
FT library, ultimately derived from placenta tissue. For a
FT detailed description of the library from which this clone
FT was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. The procedure used to
FT create this library has been previously described (Bonaldo
FT , Lennon and Soares, Genome Research 6: 791-806, 1996)
FT TAG_LIB=MI-P-Ayi TAG_TISSUE=placenta TAG_SEQ=ATTGG"
FT /organism="Sus scrofa"
FT /strain="Crossbred"
FT /clone="MI-P-Ayi-npy-e-11-0-UI"
FT /clone_lib="MI-P-Ayi"
FT /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 313 BP; 118 A; 79 C; 59 G; 57 T; 0 other;

Query Match 1.4%; Score 28.8; DB 9; Length 313;
Best Local Similarity 60.0%; Pred. No. 66;
Matches 48; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1690 TTGTATTTTCTGCTAGACAGATAACTTTTAAATTTTCAATTTGGCAGACACTTTTTT 1749
Db 107 TTCCTTTTTTTAGGAAAAAAATCCCGGAATTCCTCCCTTTTTCGAAATTTTTTTT 48
QY 1750 TTTTGTGAAATCTTTC 1769
Db 47 TTTTGTGAAATCTTTC 28

RESULT 36
HSM010170
ID HSM010170 standard; RNA; EST; 115 BP.
XX

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AC AL045320;
XX
SV AL045320.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434A125_s1 (from clone DKFZp434A125)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-115
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No r1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FT source 1..115
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434A125"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 115 BP; 7 A; 9 C; 8 G; 90 T; 1 other;
Query Match 1..115
Best Local Similarity 1.4%; Score 28.6; DB 2; Length 115;
Matches 58; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
OY 1286 CTTTGGCTTCTTCTGCTGATTTTCCCGAGATCGCATTTATTTGTTACTTTTC 1345
DB 8 CTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 67
OY 1346 TATGTATTATACTCCTGTAGAGTCACTAATAAGGAGTATTTT 1393
DB 68 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 115
RESULT 37
HSM004384/c
ID HSM004384 standard; RNA; EST; 277 BP.
XX
AC AL039908;
XX
SV AL039908.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434H0112_s1 (from clone DKFZp434H0112)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
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XX
RN [1]
RP 1-277
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT ;
RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC r1 sequence also available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FT source 1..277
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434H0112"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 277 BP; 97 A; 45 C; 19 G; 114 T; 2 other;
Query Match 1..277
Best Local Similarity 1.4%; Score 28.6; DB 2; Length 277;
Matches 85; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
OY 1613 AAAAGGTTAATGATTTTGTTCATCTCATTTGTCTATTTATCTGTATCGGTCTA 1672
DB 219 AAAAATGATGATTTCTCTGTTTGAAGAGAAGATAATTTTCTTTTAGGGAGA 160
OY 1673 AAGTGTAAATTTACCATTTGATTTTCTGTAGACAGATACTTTTAATTTTCAAT 1732
DB 159 GGTACAGTGTCTTATATTTTGGAGCTTCTGAGGTGTAATAATTTTATATCT 100
OY 1733 TGGCAGACACTTTTCTTTTCTTTTGAATACTTTCTTCCAGATCTGTGCCACTGAA 1792
DB 99 NTGAGTAAATGTTAGTAGTGTGTTTAAATACTTAATAAATAATCTTTCTCTGGA 40
RESULT 38
BF703566
ID BF703566 standard; RNA; EST; 288 BP.
XX
AC BF703566;
XX
SV BF703566.1
XX
DT 26-DEC-2000 (Rel. 66, Created)
DT 26-DEC-2000 (Rel. 66, Last updated, Version 1)
XX
DE MI-P-H1-abl-a-03-1-UM.s1 MI-P-H1 Sus scrofa cDNA clone
DE MI-P-H1-abl-a-03-1-UM 3', mRNA sequence.
XX
KW EST.
XX
OS Sus scrofa (pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
RN [1]
RP 1-288
RA MEDLINE; 97044477.
RA Ronaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL discovery";
RL Genome Res. 6(9):791-806(1996).
XX
```

```

DR UNILIB; 7279; 7279.
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142
CC Animal Science Research Center, Department of Animal Science,
CC University of Missouri-Columbia, 65211 Clone distribution: clones
CC will be available through Research Genetics (www.resgen.com) The
CC following repetitive elements were found in this cDNA sequence:
CC 1-24, >AT_richlow_complexity 85-132, >POLY_ASimple_repeat
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX Key Location/Qualifiers
FH source 1..288
FH /db_xref="taxon:9823"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-H1
FH library is derived from hypothalamus at estrus day 0. For
FH a detailed description of the library from which this
FH clone was derived, please visit our web site at
FH http://pigest.genome.iastate.edu/. TAG_SEQ=None found"
FH /organism="Sus scrofa"
FH /strain="crossbreed"
FH /clone_lib="MI-P-H1"
FH /lab_host="DH10B (Life Technologies)"
XX Sequence 288 BP; 111 A; 50 C; 7 G; 119 T; 1 other;

Query Match 1.4%; Score 28.6; DB 9; Length 288;
Best Local Similarity 51.1%; Pred. No. 73;
Matches 67; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1530 TTGCTTTTACCAACATAAGAACCATGAGTCATTTTGTCTATTAGAGTATCTGTATAA 1589
Db 1 TTTTCTTTTATTAATAAATAAACAACACCTGTTTAAATTAACCTATTTTAA 60

QY 1590 AATCTCTGAAATACAGAAATCAAAAGGTTAAATGATTTTGTTCATCTGTGTTGCA 1649
Db 61 AAAAACAACATATTTTCAAAATAATTTATTTTATTTTTCCTCAATTTTAT 120

QY 1650 TTTTATTTATCT 1660
Db 121 TTTTATTTT 131

RESULT 39
BF704175/c standard; RNA; EST; 391 BP.
XX ID BF704175
XX AC BF704175;
XX SV BF704175.1
XX DT 26-DEC-2000 (Rel. 66, Created)
XX DT 26-DEC-2000 (Rel. 66, Last updated, Version 1)
XX DE MI-P-O3-aaw-c-12-1-UM.s1 MI-P-O3 Sus scrofa cDNA clone
XX DE MI-P-O3-aaw-c-12-1-UM.3', mRNA sequence.
XX EST.
XX

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OS Sus scrofa (pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
XX RP 1-391
XX RX MEDLINE; 97044477.
XX RA Bernaldo M.F., Lennon G., Soares M.B.;
XX RT "Normalization and subtraction: two approaches to facilitate gene
XX RL discovery";
XX RL Genome Res. 6(9):791-806(1996).
XX DR UNILIB; 7285; 7285.
XX Contact: Tuggle CK
XX Molecular Genetics Laboratory, Department of Animal Science
XX Iowa State University
XX 201 Kildee Hall, Ames, IA 50011-3150, USA
XX Tel: 5152944252
XX Fax: 5152942401
XX Email: cktuggle@iastate.edu
XX The sequence contained an oligo-dT track that was present in the
XX oligonucleotide that was used to prime the synthesis of first
XX strand cDNA and therefore this may represent a bonafide poly A
XX tail. The sequence tag present in the cDNA between the NotI site
XX and the oligo-dT track served to verify it as a clone from the
XX non-normalized ovary at estrus day 12 library cDNA library
XX Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science
XX Research Center, Department of Animal Science, University of
XX Missouri-Columbia, 65211 Clone distribution: clones will be
XX available through Research Genetics (www.resgen.com)
XX Seq primer: M13 Forward
XX POLYA=Yes.
XX Key Location/Qualifiers
FH source 1..391
FH /db_xref="taxon:9823"
FH /db_xref="UNILIB:7285"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-O3
FH library is derived from ovary at estrus day 12. For a
FH detailed description of the library from which this clone
FH was derived, please visit our web site at
FH http://pigest.genome.iastate.edu/. TAG_LIB=MI-P-O3
FH TAG_TISSUE=ovary at estrus day 12 TAG_SEQ=TTGTAC"
FH /organism="Sus scrofa"
FH /strain="crossbreed"
FH /clone_lib="MI-P-O3-aaw-c-12-1-UM"
FH /lab_host="DH10B (Life Technologies)"
XX Sequence 391 BP; 155 A; 68 C; 89 G; 79 T; 0 other;

Query Match 1.4%; Score 28.6; DB 9; Length 391;
Best Local Similarity 52.0%; Pred. No. 69;
Matches 64; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1645 TGTCATTTTATTTATCTGTTATCGGTCTAAAGTGTCTAATTTTACCATTGTTTCTGCT 1704
Db 151 TTTTCTTTTCTTCTGTTATCGGTCTTAAAGTGTCTAATTTTACCATTGTTTCTGCT 92
QY 1705 AGACAGATAACTTTTAAATTTTTCAAATTTTGGCAGACACTTTTTTTTTTTTTCGAAATC 1764
Db 91 CCCCTTAAATTTTTCCTCCCAAAATTTTTCGCCCCCTTTTTCCTTTTTCCTTTAATT 32

QY 1765 TTT 1767
Db 31 TTT 29

RESULT 40
HSM001422/c

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ID HSM001422 standard; RNA; EST; 112 BP.
XX AC AL037097;
XX SV AL037097.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKF2p564L2264_r1 (from clone DKF2p564L2264)
XX KW EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX RN [1]
XX RP Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Klopferpitz 10a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No s1 sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX FH Key Location/Qualifiers
XX FT 1. .112
XX FT /db_xref="taxon:9606"
XX FT /organism="Homo sapiens"
XX FT /clone="DKF2p564L2264"
XX FT /clone_lib="564 (synonym: hfb2). Vector pAMP1; host
XX FT x1-2blue; sites NotI + SalI"
XX FT /dev_stage="fetal"
XX FT /tissue_type="brain"
XX SQ Sequence 112 BP; 77 A; 4 C; 7 G; 2 T; 22 other;

Query Match 1.4%; Score 28.4; DB 2; Length 112;
Best Local Similarity 53.4%; Pred. No. 94;
Matches 47; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 1682 TTACCATTTGATTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACA 1741
DB 89 TTTTNCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30

QY 1742 CTTTTTTTTTTTTTTGAAATCTTTCC 1769
DB 29 TTTTTTTTTTTTTTTTTTTTTTTTTTTTCC 2

RESULT 41
BF703358/c
ID BF703358 standard; RNA; EST; 245 BP.
XX AC BF703358;
XX SV BF703358.1
XX DT 26-DEC-2000 (Rel. 66, Created)
XX DT 26-DEC-2000 (Rel. 66, Last updated, Version 1)
XX DE MI-P-O3-aav-a-12-1-UM.s1 MI-P-O3 Sus scrofa cDNA clone
XX DE MI-P-O3-aav-a-12-1-UM 3', mRNA sequence.
XX KW EST.

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OS Sus scrofa (pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX RN [1]
XX RP 1-245
XX RA MEDLINE; 97044477.
XX RA Bonaldo M.F., Lennon G., Soares M.B.;
XX RT "Normalization and subtraction: two approaches to facilitate gene
XX RL discovery";
XX RL Genome Res. 6(9):791-806(1996).
XX DR UNILIB; 7285; 7285.
XX CC Contact: Tuggle CK
XX CC Molecular Genetics Laboratory, Department of Animal Science
XX CC Iowa State University
XX CC 201 Kildee Hall, Ames, IA 50011-3150, USA
XX CC Tel: 5152944252
XX CC Fax: 5152942401
XX CC Email: cktuggle@iastate.edu
XX CC The sequence contained an oligo-dT track that was present in the
XX CC oligonucleotide that was used to prime the synthesis of first
XX CC strand cDNA and therefore this may represent a bonafide poly A
XX CC tail. The sequence tag present in the cDNA between the NotI site
XX CC and the oligo-dT track served to verify it as a clone from the
XX CC non-normalized ovary at estrus day 12 library cDNA Library
XX CC Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science
XX CC Research Center, Department of Animal Science, University of
XX CC Missouri-Columbia, 55211 Clone distribution: Clones will be
XX CC available through Research Genetics (www.resgen.com) the following
XX CC repetitive elements were found in this cDNA sequence: 1-23,
XX CC >AT rich#Low complexity 24-107, >POLY_A#Simple_repeat 201-232,
XX CC >GC rich#Low complexity
XX CC Seq primer: M13 Forward
XX CC POLYA=yes.
XX FH Key Location/Qualifiers
XX FT 1. .245
XX FT /db_xref="taxon:9823"
XX FT /db_xref="UNILIB:7285"
XX FT /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
XX FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-O3
XX FT library is derived from ovary at estrus day 12. For a
XX FT detailed description of the library from which this clone
XX FT was derived, please visit our web site at
XX FT http://pigest.genome.iastate.edu/. TAG_SEQ=TTGTAC"
XX FT TAG_TISSUE=ovary at estrus day 12 TAG_SEQ=TTGTAC"
XX FT /organism="Sus scrofa"
XX FT /strain="crossbreed"
XX FT /clone_lib="MI-P-O3-aav-a-12-1-UM"
XX FT /clone_lib="MI-P-O3"
XX FT /lab_host="DH10B (Life Technologies)"
XX SQ Sequence 245 BP; 105 A; 59 C; 52 G; 29 T; 0 other;

Query Match 1.4%; Score 28.4; DB 9; Length 245;
Best Local Similarity 58.1%; Pred. No. 82;
Matches 50; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1686 CCATTTGATTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACTTT 1745
DB 109 CTTTTTTTTTTTTTCCCCCCCCCTTTTTTTTTTTTTTTGGGTTTTTAAAAAAATTT 50

QY 1746 TTTTTTTTTTTGAAATCTTTCC 1771
DB 49 TTTTTTTTTTTCTTTTTTTTATTT 24

RESULT 42
BF708447
ID BF708447 standard; RNA; EST; 273 BP.

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XX AC BF708447;  
 XX SV BF708447.1  
 XX 03-JAN-2001 (Rel. 66, Created)  
 XX 03-JAN-2001 (Rel. 66, Last updated, Version 1)  
 XX MI-P-AY0-ncm-a-02-0-UI.s1 MI-P-AY0 Sus scrofa cDNA clone  
 XX MI-P-AY0-ncm-a-02-0-UI 3', mRNA sequence.  
 XX KW EST.  
 XX Sus scrofa (pig)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 XX [1]  
 RN 1-273  
 RP MEDLINE; 97044477.  
 RX Bernaldo M.F., Lennon G., Soares M.B.;  
 RA "Normalization and subtraction: two approaches to facilitate gene  
 RT discovery";  
 RL Genome Res. 6(9):791-806(1996).  
 XX UNILIB; 7286; 7286.  
 DR  
 CC Contact: Tuggle CK  
 CC Molecular Genetics Laboratory, Department of Animal Science  
 CC Iowa State University  
 CC 201 Kildee Hall, Ames, IA 50011-3150, USA  
 CC Tel: 5152944252  
 CC Fax: 5152942401  
 CC Email: cktuggle@iastate.edu  
 CC The sequence contained an oligo-dT track that was present in the  
 CC oligonucleotide that was used to prime the synthesis of first  
 CC strand cDNA and therefore this may represent a bonafide poly A  
 CC tail. The sequence tag present in the cDNA between the NotI site  
 CC and the oligo-dT track served to verify it as a clone from the  
 CC non-normalized placenta library cDNA Library Preparation: M.B.  
 CC Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,  
 CC University of Iowa Clone distribution: clones will be available  
 CC through Research Genetics (www.resgen.com) The following repetitive  
 CC elements were found in this cDNA sequence: 113-145,  
 CC >AT-rich#Low complexity 157-207, >AT-rich#Low complexity  
 CC Seq primer: M13 Forward  
 CC POLYA=Yes.  
 XX  
 XX Key Location/Qualifiers  
 FH source 1. .273  
 FT /db\_xref="taxon:9823"  
 FT /db\_xref="UNILIB:7286"  
 FT /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-AY0  
 FT library is derived from placenta. For a detailed  
 FT description of the library from which this clone was  
 FT derived, please visit our web site at  
 FT http://pigest.genome.iastate.edu/. The procedure used to  
 FT create this library has been previously described (Bernaldo  
 FT , Lennon and Soares, Genome Research 6:791-806, 1996)  
 FT TAG LIB=MI-P-AY0 TAG TISSUE=placenta TAG\_SEQ=ATTGG"  
 FT /organisms="Sus scrofa"  
 FT /clone="MI-P-AY0-ncm-a-02-0-UI"  
 FT /clone\_lib="MI-P-AY0"  
 FT /lab\_hosts="DH10B (Life Technologies)"  
 XX  
 SQ Sequence 273 BP; 118 A; 49 C; 48 G; 58 T; 0 other;  
 Query Match 1.4%; Score 28.4; DB 9; Length 273;  
 Best Local Similarity 50.0%; Pred. No. 80;  
 Matches 71; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

. QY 1090 ATCTTCGACGACTTTGCTCACTACGAGAGCGCCAGAGGAGGAGGAGGAGGAGGAGG 1149  
 DB 62 AACCCCGGGAATTTTGGGAAAAAACAACAAACCCAAAGGGGGGAGGCCCCCAAAAAA 121  
 QY 1150 AACGGCAGAGTCGAAACAAACAAATGAGGGGGAACCCAGTTTCTTACATGTTCTAACGTTTG 1209  
 DB 122 AAAAAAATTTCTTAAAAAAGGGGGGCCAACCAATTTAAAAAATTTATTTATTTA 181  
 QY 1210 ACTTTGAAAAACAGTTTAAAAACA 1231  
 DB 182 AATAAAAAAATTTTAAAAA 203  
 RESULT 43  
 BM377646 standard; RNA; EST; 422 BP.  
 ID BM377646  
 XX AC BM377646;  
 XX SV BM377646.1  
 XX 15-JAN-2002 (Rel. 70, Created)  
 XX 15-JAN-2002 (Rel. 70, Last updated, Version 1)  
 DE EBem04 SQ003\_M04\_R IGF Barley EBem04 library Hordeum vulgare cDNA clone  
 DE EBem04\_SQ003\_M04\_5', mRNA sequence.  
 XX EST.  
 KW Hordeum vulgare  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;  
 OC Triticeae; Hordeum.  
 XX [1]  
 RN 1-422  
 RP Hedley P., Liu H., Caldwell D., McCallum N., Mudie S., Cardle L.,  
 RA Ramsay L., Machray G., Marshall D.F.M., Waugh R.;  
 RT "Development of Barley Transcriptome Resources";  
 RL Unpublished.  
 XX UNILIB; 9790; 9790.  
 DR  
 CC Contact: Waugh R  
 CC Unit of Genomics  
 CC Scottish Crop Research Institute  
 CC Invergowrie, Dundee, DD2 5DA, Scotland, UK  
 CC Tel: 00 44 1382 562731  
 CC Fax: 00 44 1382 562426  
 CC Email: tvaugh@scri.sari.ac.uk  
 CC All sequence has a Phred quality score of 20 or over  
 CC Seq primer: M13 reverse.  
 XX  
 XX Key Location/Qualifiers  
 FH source 1. .422  
 FT /db\_xref="taxon:4513"  
 FT /db\_xref="UNILIB:9790"  
 FT /note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;  
 FT Non-normalised library, directionally cloned into pSPORT1.  
 FT Derived from embryos dissected from developing grains (12  
 FT days post anthesis) in glasshouse grown barley plants.  
 FT Developed as part of the barley transcriptome resources of  
 FT BBSRC/SEERAD funded cereal IGF (Investigating Gene  
 FT Function) project."  
 FT /organism="Hordeum vulgare"  
 FT /cultivar="Optic"  
 FT /clone="EBem04\_SQ003\_M04"  
 FT /clone\_lib="IGF Barley EBem04 library"  
 FT /tissue\_type="Embryo"  
 FT /dev\_stage="12 days post anthesis"  
 FT /lab\_host="DH10B"  
 XX

[illegible]





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Db 64 CGACTGAGCGACCTCCGGCGCGCTCCGGCGCGTGCAGGTGCAGTGCAGCGCGAGATGGA 123
OY 855 GTCCCCCGTGGACTACGACACCGACCGAGTCCGGGGTCTG 890
Db 124 ATCTCTGGGTAAATTGGAGCGTGTGTAGCATATG 159

RESULT 48
AU209841/c standard; RNA; EST; 348 BP.
XX AC AU209841;
XX SV AU209841.1
XX 17-JUL-2001 (Rel. 68, Created)
XX 17-JUL-2001 (Rel. 68, Last updated, Version 1)
XX DE Caenorhabditis elegans cDNA clone:YK749d08 : 3' end, single read.
XX KW EST (expressed sequence tag).
XX OS Caenorhabditis elegans
XX OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
XX OC Rhabditidae; Peloderinae; Caenorhabditis.
XX RN 1-348
XX RA Kohara Y.;
XX RT Submitted (10-JUL-2001) to the EMBL/GenBank/DBJ databases.
XX RL Yuji Kohara, National Institute of Genetics, Genome Biology Lab.; 1111
XX RL Yata, Mishima, Shizuoka 411-8540, Japan (E-mail:ykohara@lab.nig.ac.jp,
XX RL Tel:81-559-81-6854, fax:81-559-81-6855)
XX RN [1]
XX RA Kohara Y., Shin-i T., Thierry-Mieg J., Thierry-Mieg D., Suzuki Y.,
XX RA Sugano S.;
XX RT "A complementary view of the C.elegans genome.";
XX RT Unpublished.
XX UNILIB; 9634; 9634.

Key Location/Qualifiers
FH source 1..348
FH /db_xref="taxon:6239"
FH /db_xref="UNILIB:9634"
FH /sequenced_mol="cDNA to mRNA"
FH /sex="Hermaphrodite"
FH /organism="Caenorhabditis elegans"
FH /clone="YK749d08"
FH /clone_lib="unpublished oligo-capped cDNA library"
FH /dev_stage="L1"
FH /strain="N2"
FH /tissue_type="whole animal"
XX Sequence 348 BP; 160 A; 55 C; 41 G; 85 T; 7 other;

Query Match 1.4%; Score 28; DB 3; Length 348;
Best Local Similarity 51.2%; Pred. No. 91;
Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

OY 1609 AATCAAGGTAAATGATTTTGTCTGATTTGTCATTTATATCTGTTATCTGTTATCGG 1668
Db 135 AGTCAATGGGTAAACCTACTCTTTTAAATTTTGTGTTGTTATTTGTAATAAATT 76
OY 1669 TCTAAAGTCTAATTTTACCAATTTGATTTTCTGCTAGACAGATACTTTAATTTTCA 1728
Db 75 TTTCAGCTGTAAATTTGTATTCAAATTTGTAAGTAATTTGTAATAAATTTATTTTCT 16
OY 1729 AATTT 1733

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Db 15 TCTTT 11
RESULT 49
BM832939/c standard; RNA; EST; 498 BP.
XX BM832939;
XX AC BM832939.1
XX SV BM832939.1
XX 10-MAR-2002 (Rel. 71, Created)
XX 10-MAR-2002 (Rel. 71, Last updated, Version 1)
XX DE K-EST0107506 S5SNU484s1 Homo sapiens cDNA clone S5SNU484s1-10-E02 5', mRNA
XX KW sequence.
XX EST.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX RN [1]
XX RA Kim N.S., Hahn Y., Oh J.H., Lee J.Y., Ahn H.Y., Chu M.Y., Kim M.R.,
XX RA Oh K.J., Cheong J.E., Sohn H.Y., Kim J.M., Park H.S., Kim S., Kim Y.S.;
XX RT "21C Frontier Korean EST Project 2001";
XX RT Unpublished.
XX UNILIB; 10302; 10302.

Key Location/Qualifiers
FH source 1..498
FH /db_xref="taxon:9606"
FH /db_xref="UNILIB:10302"
FH /note="Organ: Stomach; Vector: pTZ18RPI; Site_1: EcoRI;
FH Site_2: NotI; The poly (A)+ RNA was decapped with tobacco
FH acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
FH including EcoRI site by treatment of T4 RNA ligase. The
FH first strand cDNA was synthesized from oligo dT-selected
FH mRNA by priming with dT-tailed vector. The dT-tailed vector
FH was adjusted to have about 60nt. The cDNA vector was
FH circularized with E. coli DNA ligase after digestion of
FH EcoRI which site is also included in vector. An RNA strand
FH converted to a DNA strand by Okayama-Berg method. The
FH obtained cDNA vectors were used for transformation of
FH competent cells E. coli Top10F' by electroporation method.
FH After analyzing and sequencing about 2,000 ~ 3,000 colonies
FH in original cDNA library, the abundant cDNAs were selected
FH and amplified by PCR reaction using vector region primer
FH including T7 promoter as 5' primer and N(dT)14 as 3'
FH primer. The PCR products were used as template for
FH synthesis of biotinylated single stranded RNA by in vitro
FH transcription reaction. The synthesized RNA probes were
FH hybridized with antisense single stranded cDNAs prepared
FH from original library and incubated with avidin-gel. After
FH removing DNA-RNA hybrids by centrifuge, the subtracted cDNA
FH libraries were constructed by transformation of the
FH remaining DNA into competent cells E. coli Top10F' with
FH electroporation method."

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FT /sex="M"
FT /organism="Homo sapiens"
FT /clones="SSNU484s1-10-E02"
FT /clone_lib="SSNU484s1"
FT /tissue_type="Stomach"
FT /cell_type="Epithelial"
FT /cell_line="SNU-484"
FT /lab_host="Top10P"
SQ Sequence 498 BP; 167 A; 90 C; 87 G; 154 T; 0 other;

Query Match      1.4%; Score 28; DB 2; Length 498;
Best Local Similarity 50.8%; Pred. No. 85;
Matches 67; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1650 TTTTATTATCTGTTATCGTCTAAAGTCCTAATTACCACTTTGATTTCTGCTAGACA 1709
Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1710 GATAACTTTTAAATTTTCAAAATTTGGCAGACACTTTTTTTTTTTTTTGAATACTTTCC 1769
Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dd 287 TTTTCTTTTACAGGTATTCATTTCTGTAGAAAATTCGAAATATTTATTTTAAATTTTAC 228
QY 1770 TTCAGATCTGT 1781
Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dd 227 ATTTGGGTCTGT 216

RESULT 50
BF713161/c standard; RNA; EST; 522 BP.
XX BF713161;
XX BF713161;
SV BF713161.1
XX 03-JAN-2001 (Rel. 66, Created)
DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX MI-P-O1-adq-a-12-1-UM.s1 MI-P-O1 Sus scrofa cDNA clone
DE MI-P-O1-adq-a-12-1-UM 3', mRNA sequence.
XX MI-P-O1-adq-a-12-1-UM 3', mRNA sequence.
XX EST.
XX Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
XX 1-522
XX MEDLINE; 97044477.
XX Ronaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL discovery";
RL Genome Res. 6(9):791-806(1996).
XX UNILIB; 7283; 7283.
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized ovary at estrus day 0 library cDNA Library
CC Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science
CC Research Center, Department of Animal Science, University of

```

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CC Missouri-Columbia, 65211 Clone distribution: clones will be
CC available through Research Genetics (www.resgen.com)
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX Key Location/Qualifiers
FH 1..522
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7283"
FT /notes="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-O1
FT library is derived from ovary at estrus day 0. For a
FT detailed description of the library from which this clone
FT was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. TAG LIB=MI-P-O1
FT TAG_TISSUE=ovary at estrus day 0 TAG_SEQ=GACGTA"
FT /organism="Sus scrofa"
FT /strain="crossbred"
FT /clone="MI-P-O1-adq-a-12-1-UM"
FT /clone_lib="MI-P-O1"
FT /lab_host="DH10B (Life Technologies)"
XX Sequence 522 BP; 176 A; 91 C; 131 G; 123 T; 1 other;

Query Match      1.4%; Score 28; DB 9; Length 522;
Best Local Similarity 52.6%; Pred. No. 84;
Matches 61; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 1876 TTAGCTCTGTTTCCAGGTCGGGCACTCTTTGTTGTTGCACTTTTAAATTTTACAC 1935
Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dd 463 TGAAGCCTTCCTCGCGGCTGGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 404
QY 1936 CTTTCTTAAAGATTTCTAATGCGCTTAAAGTTTATATACCAATATGCTGAGCTT 1991
Dd ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dd 403 TTTTCTAATGGATTCAGGACTTTTATATCTCATAGCTATCCAGCTCCACTT 348

RESULT 51
BF702115 standard; RNA; EST; 337 BP.
XX BF702115;
XX BF702115;
SV BF702115.1
XX 25-DEC-2000 (Rel. 66, Created)
DT 25-DEC-2000 (Rel. 66, Last updated, Version 1)
XX MI-P-Al-aap-a-08-1-UM.s1 MI-P-Al Sus scrofa cDNA clone
DE MI-P-Al-aap-a-08-1-UM 3', mRNA sequence.
XX MI-P-Al-aap-a-08-1-UM 3', mRNA sequence.
XX EST.
XX Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
XX 1-337
XX MEDLINE; 97044477.
XX Ronaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL discovery";
RL Genome Res. 6(9):791-806(1996).
XX UNILIB; 7271; 7271.
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252

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CC The sequence contained an oligo-dT track that was present in the  
 CC oligonucleotide that was used to prime the synthesis of first  
 CC strand cDNA and therefore this may represent a bonafide poly A  
 CC tail. The sequence tag present in the cDNA between the NotI site  
 CC and the oligo-dT track served to verify it as a clone from the  
 CC normalized placenta library cDNA Library Preparation: M.B. Soares  
 CC Lab, University of Iowa EST sequencing: M.B. Soares Lab, University  
 CC of Iowa Clone Distribution: clones will be available through  
 CC Research Genetics (www.resgen.com) The following repetitive  
 CC elements were found in this cDNA sequence: 54-172,  
 CC >POLY\_A\$Simple\_repeat 193-274, >POLY\_A\$Simple\_repeat  
 CC Seq primer: M13 Forward  
 CC POLYA=yes.

XX Key Location/Qualifiers

XX 1. 522

XX /db\_xref="taxon:9823"

XX /db\_xref="UNILIB:7287"

XX /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 XX polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-AV1  
 XX library is normalized library derived from the MI-P-AV1  
 XX library, ultimately derived from placenta tissue. For a  
 XX detailed description of the library from which this clone  
 XX was derived, please visit our web site at  
 XX http://pigest.genome.iastate.edu/. The procedure used to  
 XX create this library has been previously described (Bonaldo  
 XX . Lennon and Soares, Genome Research 6: 791-806, 1996)  
 XX TAG\_LIB=MI-P-AV1 TAG\_TISSUE=placenta TAG\_SEQ=ATTGCG"  
 XX /organism="Sus scrofa"  
 XX /strain="crossbreed"  
 XX /clone="MI-P-AV1-ngh-a-08-0-UI"  
 XX /clone\_lib="MI-P-AV1"  
 XX /lab\_host="DH10B (Life Technologies)"

XX Sequence 522 BP; 255 A; 108 C; 85 G; 74 T; 0 other;

Query Match 1.4%; Score 27.6; DB 9; Length 522;  
 Best Local Similarity 50.8%; Pred. No. 99;  
 Matches 66; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

OY 1638 TCTGATTGTCATTATATCTGTTATCGTCTAAGTCTAAAGTCTAATTTACCATTTGATTT 1697

Db 174 TATTTTTCCTCCCTTTTATTTTATTTTGAACCATGGGTATTTTATTTTGTGTTA 115

OY 1698 TTCTGCTAGACAGACTACTTTTAAATTTTCAATTTGGCAGACACTTTTATTTT 1757

Db 114 GGTTTTTCCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 55

OY 1758 GAAATCTTT 1767

Db 54 TGGGAATTTT 45

RESULT 60

BM818575/c

ID BM818575 standard; RNA; EST; 569 BP.

XX AC BM818575;

XX SV BM818575.1

XX DT 10-MAR-2002 (Rel. 71, Created)

XX DT 10-MAR-2002 (Rel. 71, Last updated, Version 1)

DE K-EST0085904 S21SNU520s1 Homo sapiens cDNA clone S21SNU520s1-4-F12 5', mRNA  
 DE sequence.

XX EST.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX 1-569

RN Kim N.S., Hahn Y., Oh J.H., Lee J.Y., Ahn H.Y., Chu M.Y., Kim M.R.,  
 RA Oh K.J., Cheong J.B., Sohn H.Y., Kim J.M., Park H.S., Kim Y.S.;  
 RT "21C Frontier Korean EST Project 2001";  
 RL Unpublished.

XX UNILIB; 10325; 10325.

XX Contact: Kim YS

CC Genome Research Center

CC Korea Research Institute of Bioscience & Biotechnology

CC 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

CC Tel: +82-42-860-4470

CC Fax: +82-42-860-4409

CC Email: yongsung@mail.kribb.re.kr

CC Plate: 4 row; F column: 12

CC High quality sequence stop: 569.

XX Key Location/Qualifiers

XX 1. 569

XX /db\_xref="taxon:9606"

XX /db\_xref="UNILIB:10325"

XX /note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;  
 XX Site 2: NotI; The poly (A)+ RNA was dephosphorylated with  
 XX bacterial alkaline phosphatase (BAP) and then decapped with  
 XX tobacco acid pyrophosphatase (TAP). The decapped intact  
 XX mRNA was ligated with DNA-RNA linker including EcoR I site  
 XX by treatment of T4 RNA ligase and the first strand cDNA was  
 XX synthesized from oligo dT-selected mRNA by priming with  
 XX dT-tailed vector. The dT-tailed vector was adjusted to have  
 XX about 60nt. The cDNA vector was circularized with E. coli  
 XX DNA ligase after digestion of EcoRI which site is also  
 XX included in vector. An RNA strand converted to a DNA strand  
 XX by Okayama-Berg method. The obtained cDNA vectors were used  
 XX for transformation of competent cells E. coli Top10P' by  
 XX electroporation method. The cDNA libraries constructed by  
 XX this method are full-length enriched cDNA library. After  
 XX analyzing and sequencing about 2,000 ~ 3,000 colonies in  
 XX original cDNA library, the abundant cDNAs were selected and  
 XX amplified by PCR reaction using vector region primer  
 XX including T7 promotor as 5' primer and N(DT)14 as 3'  
 XX primer. The PCR products were used as template for  
 XX synthesis of biotinylated single stranded RNA by in vitro  
 XX transcription reaction. The synthesized RNA probes were  
 XX hybridized with antisense single stranded cDNAs prepared  
 XX from original library and incubated with avidin-gel. After  
 XX removing DNA-RNA hybrids by centrifuge, the subtracted cDNA  
 XX libraries were constructed by transformation of the  
 XX remaining DNA into competent cells E. coli Top10P' with  
 XX electroporation method."

XX /sex="F"

XX /organism="Homo sapiens"

XX /clone="S21SNU520s1-4-F12"

XX /clone\_lib="S21SNU520s1"

XX /tissue\_type="Stomach"

XX /cell\_type="Floating aggregates"

XX /cell\_line="SNU-520"

XX /lab\_host="Top10P'"

XX Sequence 569 BP; 183 A; 122 C; 137 G; 127 T; 0 other;

Query Match 1.4%; Score 27.6; DB 2; Length 569;  
 Best Local Similarity 49.3%; Pred. No. 98;  
 Matches 72; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

OY 1626 TTTTGTTCATTCGATTTGTCATTTTATTTATCTGTTATCGTCTAAAGTCTAATTTA 1685

Db 416 TTTTGTTCATTCGATTTGTCATTTTATTTTATTTTATTTTATTTTATTTTATTTT 357

OY 1686 CCCATTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTT 1745

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Db 356 ATTAATAGCTGCAGTCTCAAAATCTTTTCATCATCAGATGTTTGGCGAAGTTT 297
Qy 1746 TTTTTCATTTTGAATCTTTTCCTT 1771
Db 296 GGCCTTCTAGTGTGAACCTGGACCTT 271

RESULT 61
HSM012004
ID HSM012004 standard; RNA; EST; 647 BP.
XX AC AL047154;
XX SV AL047154.1
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp566E2018_r1 (from clone DKFZp566E2018)
XX KW EST; expressed sequence tag.
XX OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
RN 1-647
RA Wambutt R., Heubner D., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by AGOWA within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX PH Key Location/Qualifiers
FH source 1..647
FT /db xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp566E2018"
FT /clone_lib="586 (synonym: hutel). Vector pSport1; host
FT DH10B; sites NotI + SalI/MluI"
FT /dev_stage="adult"
FT /tissue_type="uterus"
XX SQ Sequence 647 BP; 220 A; 94 C; 124 G; 206 T; 3 other;

Query Match 1.4%; Score 27.6; DB 2; Length 647;
Best Local Similarity 50.8%; Pred. No. 95;
Matches 66; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 1557 TGAGTCTATTTGTCTATTTAGAGTATCTTGATAAAATCTTTGAAAATCTCAAAATCAAAA 1616
Db 297 TCATCCATATCATCTTATGACAGAGGCGAGTGTGTTTATCTTTGGAAATTAAAG 356

Qy 1617 GGTTAATGATTTTGTTCATCTGATTGTTCATTTTATTTATCTGTTATCGGTCTAAAGT 1676
Db 357 ATTAACAAGTTTGGACAATATTGTTTTTATTTTAAATTTTAAATTTGAAAATAATAA 416

Qy 1677 GCTAATTAC 1686
Db 417 ATTAATAATAC 426

RESULT 62
HSM003964
ID HSM003964 standard; RNA; EST; 798 BP.
XX AC AL039488;
XX SV AL039488.1
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434A1311_s1 (from clone DKFZp434A1311)
XX KW EST; expressed sequence tag.
XX OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
RN 1-798
RA Duysterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC r1 sequence also available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX PH Key Location/Qualifiers
FH source 1..798
FT /db xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434A1311"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX SQ Sequence 798 BP; 210 A; 200 C; 183 G; 202 T; 3 other;

Query Match 1.4%; Score 27.6; DB 2; Length 798;
Best Local Similarity 63.6%; Pred. No. 92;
Matches 42; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 1570 CATTAGAGTATTTCTGATAAAATCTTTGAAAATCTCAAAATCAAAAGTTAATGATTTT 1629
Db 145 CAAATTCAGTGTGTGAGAAAACCTGGTAACCATGCAGAAATTTTAAACATCTATGAATTT 204

Qy 1630 TTGTTC 1635
Db 205 TTTTTC 210

RESULT 63
HSM001209/C
ID HSM001209 standard; RNA; EST; 125 BP.
XX AC AL036892;
XX SV AL036892.1
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp564A1064_r1 (from clone DKFZp564A1064)
XX KW EST; expressed sequence tag.
XX OS Homo sapiens (human)

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CC Research Center, Department of Animal Science, University of
CC Missouri-Columbia, 65211 Clone distribution: clones will be
CC available through Research Genetics (www.resgen.com) The following
CC repetitive elements were found in this cDNA sequence: 1-46,
CC >AT-rich/low complexity
CC Seq primer: M13 Forward
CC POLYA=yes.
XX
XX
FH Key Location/Qualifiers
FH source 1. .380
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7285"
FT /notes="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not 1; Site 2: EcoRI; The M1-P-03
FT library is derived from ovary at estrus day 12. For a
FT detailed description of the library from which this clone
FT was derived, please visit our web site at
FT http://pigest.genome.istate.edu/. TAG LIB=M1-P-03
FT TAG TISSUE=ovary at estrus day 12 TAG_SEQ=TTGTAC"
FT /organism="Sus scrofa"
FT /strain="crossbreed"
FT /clone="MI-P-03-abc-e-02-1-UM"
FT /clone_lib="MI-P-03"
FT /lab_hosts="DH10B (Life Technologies)"
XX
SQ Sequence 380 BP; 124 A; 50 C; 67 G; 139 T; 0 other;
Query Match 1.4%; Score 27.4; DB 9; Length 380;
Best Local Similarity 52.1%; Pred. No. 1.1e+02;
Matches 85; Conservative 0; Mismatches 76; Indels 2; Gaps 1;
QY 1391 TTTTGTGAGCTTATCAATCAGCTGATGATGTAATGTGAATGTAATGCTTTAAAAACAAA 1450
DB 162 TATTTTCTGCTGTTTACTTTCAGTGCCATAAAGCCATATGCTATACATTAAGCCCAAG 103
QY 1451 GCATCTATTTGGCAGAAATGTTCTTAAATTCAGTCATTTGATGATTCGTGAGACTT 1510
DB 102 ACATGGATGTTTAAAGAAATTAATGTTTAA--CAGTTTCACTGATGCTTTCACACTA 45
QY 1511 CATATTTCTATCCCTTTATTCCTTTTATAGCAACATAGAAA 1553
DB 44 TTTTATTAATAAATCATATATTTGCTTAAAAAAAATAAAAAA 2
RESULT 66
BM372823/c standard; RNA; EST; 402 BP.
ID BM372823
AC
XX
AC
XX
SV BM372823.1
XX
DT 16-JAN-2002 (Rel. 70, Created)
DT 16-JAN-2002 (Rel. 70, Last updated, Version 1)
XX
EBma04 SQ002_A22 R IGF Barley EBma04 library Hordeum vulgare cDNA clone
DE EBma04_SQ002_A22_5', mRNA sequence.
XX
XX
XX EST.
XX
XX
OS Hordeum vulgare
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
XX
XX [1]
RN Hedley P., Liu H., Caldwell D., McCallum N., Mudie S., Cardle L.,
RA Ramsay L., Machray G., Marshall D.F.M., Waugh R.;
RT "Development of Barley Transcriptome Resources";
RL Unpublished.
XX

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```

DR UNILIB; 10113; 10113.
XX
XX Contact: Waugh R
CC Unit of Genomics
CC Scottish Crop Research Institute
CC Invergowrie, Dundee, DD2 5DA, Scotland, UK
CC Tel: 00 44 1382 562731
CC Fax: 00 44 1382 562426
CC Email: rwaugh@scri.saxi.ac.uk
CC All sequence has a Phred quality score of 20 or over
CC Seq primer: M13 reverse.
XX
XX Key Location/Qualifiers
FH source 1. .402
FT /db_xref="taxon:4513"
FT /db_xref="UNILIB:10113"
FT /notes="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
FT Non-normalised library, directionally cloned into pSPORT1.
FT Derived from maternal tissue dissected from developing
FT grains (10 days post anthesis) in glasshouse grown barley
FT plants. Developed as part of the barley transcriptome
FT resources of BSRG/SEERAD funded cereal IGF (investigating
FT Gene Function) project."
FT /organism="Hordeum vulgare"
FT /cultivar="Optic"
FT /clone="EBma04 SQ002_A22"
FT /clone_lib="IGF Barley EBma04 library"
FT /tissue_type="Maternal tissue"
FT /dev_stage="10 days post anthesis"
FT /lab_hosts="DH10B"
XX
SQ Sequence 402 BP; 84 A; 117 C; 104 G; 97 T; 0 other;
Query Match 1.4%; Score 27.4; DB 6; Length 402;
Best Local Similarity 49.0%; Pred. No. 1.1e+02;
Matches 73; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 696 CGACATCCACCGCTCCATTAACTACTCCATCTGCTGTAGCAGCAGCAGCAACAGCG 755
DB 174 CGGGCTCGTCCGCTGCGAGGGGCATCCGAGCTGGGGAGCATCGCCCTGCTCTCTGCA 115
QY 756 CTGTGACAGCGCTTTCGCTGCTGATGACAGCAAGGGCCGCTCTACCTGCTCTTCAGCGT 815
DB 114 TCGAGCTTGATTTCAGCGGAGCATCGGCCCTGCGCGCTGCTGAGCAGCCTCCATGGAGT 55
QY 816 CAATGGGAGTGGGCATTTTGTGGGGTG 844
DB 54 CGATGATCTCTCGATCCTCTTGAGTCG 26
RESULT 67
BM370203
ID BM370203 standard; RNA; EST; 437 BP.
XX
AC
XX
AC
XX
SV BM370203.1
XX
DT 16-JAN-2002 (Rel. 70, Created)
DT 16-JAN-2002 (Rel. 70, Last updated, Version 1)
XX
EBro08 SQ003_E22 R IGF Barley EBro08 library Hordeum vulgare cDNA clone
DE EBro08_SQ003_E22_5', mRNA sequence.
XX
XX EST.
XX
XX
OS Hordeum vulgare
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
XX
XX [1]
RN

```

RP 1-437 Hedley P., Liu H., Caldwell D., McCallum N., Mudie S., Cardle L.,  
RA Ramsey L., Machray G., Marshall D.F.M., Waugh R.,  
RT "Development of Barley Transcriptome Resources";  
RL Unpublished.  
XX UNILIB; 9796; 9796.  
DR Contact: Waugh R  
XX Unit of Genomics  
CC Scottish Crop Research Institute  
CC Invergowrie, Dundee, DD2 5DA, Scotland, UK  
CC Tel: 00 44 1382 562731  
CC Fax: 00 44 1382 562426  
CC Email: rwaugh@scri.sari.ac.uk  
CC All sequence has a Phred quality score of 20 or over  
CC Seq primer: M13 reverse.  
XX Key Location/Qualifiers  
FH 1. .437  
FT /db\_xref="taxon:4513"  
FT /db\_xref="UNILIB:9796"  
FT /note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;  
FT Non-normalised library, directionally cloned into pSPORT1.  
FT Derived from roots of 3 week old drought stressed barley  
FT plants. Developed as part of the barley transcriptome  
FT resources of BBSRC/SEERAD funded cereal IGF (Investigating  
FT Gene Function) project."  
FT /organism="Hordeum vulgare"  
FT /cultivar="Optic"  
FT /clone="EBro08\_SQ003\_E22"  
FT /clone\_lib="IGF Barley EBro08 library"  
FT /tissue\_type="Drought stressed root"  
FT /lab\_host="DH108"  
XX Sequence 437 BP; 99 A; 111 C; 98 G; 129 T; 0 other;  
XX  
XX Query Match 1.4%; Score 27.4; DB 6; Length 437;  
XX Best Local Similarity 51.2%; Pred. No. 1.1e+02;  
XX Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
QY 1657 ATCTGTATCGGTCTAAGTCTAAATTTACCCATTTGATTTTCTGTCAGACATAACT 1716  
DB 258 AGCCGTCATGATACATAGAGTATCTCACCTTTTCTCTCTCTCTCTCTCTCTCTCT 317  
QY 1717 TTTAATTTTCAATTTGGCAGACACTTTTCTTTTGTGAAATCTTCTCTCCAGA 1776  
DB 318 TCATCT 377  
QY 1777 TCTGT 1781  
DB 378 GCTGT 382  
XX  
XX RESULT 68  
XX BM854730/c  
ID BM854730 standard; RNA; EST; 604 BP.  
XX  
XX AC BM854730;  
XX  
XX SV BM854730.1  
XX  
XX 11-MAR-2002 (Rel. 71, Created)  
DT 11-MAR-2002 (Rel. 71, Last updated, Version 1)  
XX  
XX K-EST0137384 S14K402 Homo sapiens cDNA clone S14K402-35-H10 5', mRNA  
DE sequence.  
DE  
XX KW EST.  
XX  
XX Homo sapiens (human)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
XX [1]  
RN 1-604  
RP Kim N.S., Hahn Y., Oh J.H., Lee J.Y., Ahn H.Y., Chu M.Y., Kim M.R.,  
RA Oh K.J., Cheong J.E., Sohn H.Y., Kim J.M., Park H.S., Kim S., Kim Y.S.;  
RT "21C Frontier Korean EST Project 2001";  
RL Unpublished.  
XX UNILIB; 10316; 10316.  
DR Contact: Kim YS  
XX Genome Research Center  
CC Korea Research Institute of Bioscience & Biotechnology  
CC 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
CC Tel: +82-42-860-4470  
CC Fax: +82-42-860-4409  
CC Email: yongsung@mail.kribb.re.kr  
CC Plate: 35 row; H column: 10  
CC High quality sequence stop: 604.  
XX Key Location/Qualifiers  
FH 1. .604  
FT /db\_xref="taxon:9606"  
FT /db\_xref="UNILIB:10316"  
FT /note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;  
FT Site 2: NotI; The poly (A) + RNA was dephosphorylated with  
FT bacterial alkaline phosphatase (BAP) and then decapped with  
FT tobacco acid pyrophosphatase (TAP). The decapped intact  
FT mRNA was ligated with DNA-RNA linker including EcoRI site  
FT by treatment of T4 RNA ligase and the first strand cDNA was  
FT synthesized from oligo dt-selected mRNA by priming with  
FT dt-tailed vector. The dt-tailed vector was adjusted to have  
FT about 60nt. The cDNA vector was circularized with E. coli  
FT DNA ligase after digestion of EcoRI which site is also  
FT included in vector. An RNA strand converted to a DNA strand  
FT by Okayama-Berg method. The obtained cDNA vectors were used  
FT for transformation of competent cells E. coli Top10<sup>8</sup> by  
FT electroporation method. The cDNA libraries constructed by  
FT this method are full-length enriched cDNA library."  
FT /organism="Homo sapiens"  
FT /clone="S14K402-35-H10"  
FT /clone\_lib="S14K402"  
FT /cell\_lines="K402"  
FT /lab\_host="Top10<sup>8</sup>"  
XX  
XX Sequence 604 BP; 170 A; 181 C; 148 G; 105 T; 0 other;  
XX  
XX Query Match 1.4%; Score 27.4; DB 2; Length 604;  
XX Best Local Similarity 57.6%; Pred. No. 1e+02;  
XX Matches 49; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 1711 ATAACTTTTAAATTTTCAATTTGGCAGACACTTTTCTTTTGTGAAATCTTCTCT 1770  
DB 499 ATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 440  
QY 1771 TCCAGATCTGTTGCCCACTGACAG 1795  
DB 439 TTTTGAICAGTTTTCAGGGGACAG 415  
XX  
XX RESULT 69  
XX HSM002724/c  
ID HSM002724 standard; RNA; EST; 680 BP.  
XX  
XX AC AL038379;  
XX  
XX SV AL038379.1  
XX  
XX 12-MAR-1999 (Rel. 59, Created)  
DT 25-SEP-1999 (Rel. 61, Last updated, Version 3)  
XX



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RESULT 71
HSC2714/c standard; RNA; EST; 382 BP.
XX
AC C04271;
XX
SV C04271.1
XX
DT 29-JUL-1996 (Rel. 48, Created)
DT 29-JUL-1996 (Rel. 48, Last updated, Version 1)
XX
DE Human Heart cDNA, clone 3NH3039.
XX
KW EST(expressed sequence tag).
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
RP 1-382
RA Nakamura Y.;
RT
RL Submitted (22-FEB-1996) to the EMBL/GenBank/DBJ databases.
RL Yusuke Nakamura, Institute of Medical Science, The University of Tokyo,
RL Laboratory of Molecular Medicine; 4-6-1, Shirokanedai, Minato-ku, Tokyo
RL 108, Japan (E-mail:Yusuke@ims.u-tokyo.ac.jp, Tel:81-3-5449-5372,
RL Fax:81-3-5449-5433)
XX
RN [2]
RP 1-382
RA Tanaka T., Ogiwara A., Uchiyama I., Takagi T., Yazaki Y., Nakamura Y.;
RT "Construction of a Normalized Directionally Cloned cDNA Library from Adult
RT Heart and Analysis of 3040 Clones by Partial Sequencing";
RL Genomics 35:231-235(1996).
XX
FH Key Location/Qualifiers
FT source 1..382
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /dev_stage="Adult"
FT /tissue_type="Heart"
XX
SQ Sequence 382 BP; 128 A; 136 C; 22 G; 95 T; 1 other;
Query Match 1..382 Score 27.2; DB 2; Length 382;
Best Local Similarity 56.8%; Pred. No. 1.2e+02;
Matches 50; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 1824 GATTGGCTGGATGGTGGGCATGATGTCGAGGAACTGGAGGTCCTTGGTCT 1883
DB 271 GATTGGGAGGATCCTATGTTGGTGGGGCTTGTATGATTATGGGGCTGATTAGTAGT 212
QY 1884 GGTTACGGTGGGCATCTTTTGTGT 1911
DB 211 AGTTACTGGTTGAACATGTTTGTGCT 184
RESULT 72
AU218039/c standard; RNA; EST; 571 BP.
XX
AC AU218039;
XX
SV AU218039.1
XX
DT 17-JUL-2001 (Rel. 68, Created)
DT 17-JUL-2001 (Rel. 68, Last updated, Version 1)
XX
DE Caenorhabditis elegans cDNA clone:yk859c04 : 3' end, single read.
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XX EST (expressed sequence tag).
KW Caenorhabditis elegans
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
XX
RN [1]
RP 1-571
RA Kohara Y.;
RT
RL Submitted (10-JUL-2001) to the EMBL/GenBank/DBJ databases.
RL Yuji Kohara, National Institute of Genetics, Genome Biology Lab.; 1111
RL Yata, Mishima, Shizuoka 411-8540, Japan (E-mail:ykohara@lab.nig.ac.jp,
RL Tel:81-559-81-6854, Fax:81-559-81-6855)
XX
RN [2]
RA Kohara Y., Shin-i T., Thierry-Mieg J., Thierry-Mieg D., Suzuki Y.,
RA Sugano S.;
RT "A complementary view of the C.elegans genome.";
RL Unpublished.
XX
DR UNILIB; 9634; 9634.
XX
FH Key Location/Qualifiers
FT source 1..571
FT /db_xref="taxon:6239"
FT /db_xref="UNILIB:9634"
FT /sequenced_mol="cDNA to mRNA"
FT /sex="Hermaphrodite"
FT /organism="Caenorhabditis elegans"
FT /clone_lib="unpublished oligo-capped cDNA library"
FT /dev_stage="L1"
FT /strain="N2"
FT /tissue_type="whole animal"
XX
SQ Sequence 571 BP; 195 A; 123 C; 114 G; 138 T; 1 other;
Query Match 1..571 Score 27.2; DB 3; Length 571;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Matches 56; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 1881 TCTGGTTCAGGGTCGGGCATCTCTTGTGTTGTCATCTTTTAAATTTTACACCTTT 1940
DB 105 TTGTGATGAGTTTGTGCTTTTAAAGAAATCTTTTATTATTATTTCCAAATTC 46
QY 1941 CTTAAGAAATCTAATGCCGCTTAAGTTTATACCAATAAGCT 1985
DB 45 CTTTCCATTTTCTTCGCTCACTAAATTTAAATAAAAAAANCT 1
RESULT 73
HSM010819 standard; RNA; EST; 125 BP.
XX
AC AL045969;
XX
SV AL045969.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434N226_s1 (from clone DKFZp434N226)
XX
KW EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1]
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RP 1-125  
RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;  
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases:  
RL MIPs, Am Klopferpitz 18a D-82152 Martinsried, GERMANY  
XX  
CC Clone from S. Wiemann, sequenced by BMFZ within the cDNA  
CC sequencing consortium of the German Genome Project  
CC r1 sequence is also available  
CC This clone is available at the RZPD in Berlin  
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
CC Berlin-Charlottenburg, GERMANY; Email: clone@zpd.de  
XX  
FH Key Location/Qualifiers  
FH source 1. .125  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone="DKFZp5660182"  
FT /DH10B; sites NotI + SalI  
FT /dev stage="adult"  
FT /tissue\_type="testis"  
SQ Sequence 125 BP; 1 A; 4 C; 5 G; 113 T; 2 other;  
  
Query Match 1.3%; Score 27; DB 2; Length 125;  
Best Local Similarity 51.3%; Pred. No. 1.7e+02;  
Matches 60; Conservative 0; Mismatches 57; Indels 0; Gaps 0;  
  
Qy 1626 TTTTGTGTCATTCGATTTCTGCAATTTTATTCATCGTATCGGTCTAAAGTCTAATTTA 1685  
Db 7 TTTTGTGTCATTCGATTTCTGCAATTTTATTCATCGTATCGGTCTAATTTA 66  
  
Qy 1686 CCCATTTGATTTTCTGCTACAGATTAATTTTCAATTTTGGCAGACAC 1742  
Db 67 TTTTGTGTCATTCGATTTCTGCAATTTTATTCATCGTATCGGTCTAATTTA 123  
  
RESULT 74  
HSM002746/c  
ID HSM002746 standard; RNA; EST; 265 BP.  
XX  
AC AL038400;  
XX  
SV AL038400.1  
XX  
DT 12-MAR-1999 (Rel. 59, Created)  
DT 25-SEP-1999 (Rel. 61, Last updated, Version 3)  
XX  
DE Homo sapiens mRNA; EST DKFZp5660182\_s1 (from clone DKFZp5660182)  
XX  
KW EST; expressed sequence tag.  
XX  
XX Homo sapiens (human)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
XX  
XX [1]  
RN 1-265  
RP Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;  
RA Submitted (24-SEP-1999) to the EMBL/GenBank/DBJ databases.  
RL MIPs, Am Klopferpitz 18a, D-82152 Martinsried, GERMANY  
XX  
XX RZPD; DKFZp5660182; DKFZp5660182.  
XX  
CC This is the 3' sequence of the clone insert  
CC Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
CC Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;  
CC sequenced by MediGenomix within the cDNA sequencing consortium  
CC of the German Genome Project.  
CC No r1 sequence available.

CC This clone is available at the RZPD in Berlin.  
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,  
CC 14059 Berlin-Charlottenburg, GERMANY; Email: clone@zpd.de  
XX  
XX Key Location/Qualifiers  
FH source 1. .265  
FT /db\_xref="taxon:9606"  
FT /db\_xref="RZPD:DKFZp5660182"  
FT /organism="Homo sapiens"  
FT /clone="DKFZp5660182"  
FT /clone\_lib="566 (synonym: hfk2). Vector pAMP1; host  
FT X1-2blue; sites NotI + SalI"  
FT /dev stage="fetal"  
FT /tissue\_type="kidney"  
XX  
SQ Sequence 265 BP; 101 A; 37 C; 21 G; 106 T; 0 other;  
  
Query Match 1.3%; Score 27; DB 2; Length 265;  
Best Local Similarity 49.6%; Pred. No. 1.4e+02;  
Matches 69; Conservative 0; Mismatches 70; Indels 0; Gaps 0;  
  
Qy 1534 TTTTACCAACATAGAAACCATGAGTCATTTTGTTCATTTAGAGTATCTGATAAAATC 1593  
Db 219 TTTTATAAGACTACTATACAACTACAGAGTTTATGATTAAGGTACTTAAAGCTTCTA 160  
  
Qy 1594 TCTTGAATACTCGAAATCAAAAGTTAAATGATTTTTTGTTCATTTGATTTGTCATTTT 1653  
Db 159 TGGTGCATTTGATATATATATTTTAAAGGTTTCTATATGGGATTTTCTATTTA 100  
  
Qy 1654 ATTATCTGTTATCGGTCTA 1672  
Db 99 TGTAGTAAATATGTTCTA 81  
  
RESULT 75  
BF703011/c  
ID BF703011 standard; RNA; EST; 649 BP.  
XX  
AC BF703011;  
XX  
SV BF703011.1  
XX  
DT 26-DEC-2000 (Rel. 56, Created)  
DT 26-DEC-2000 (Rel. 66, Last updated, Version 1)  
XX  
DE MI-P-E5-abn-a-08-1-UM.s1 MI-P-E5 Sus scrofa cDNA clone  
DE MI-P-E5-abn-a-08-1-UM 3', mRNA sequence.  
XX  
KW EST.  
XX  
OS Sus scrofa (pig)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
XX  
XX [1]  
RN 1-649  
RP MEDLINE; 97044477.  
RA Ronaldo M.F., Lennon G., Soares M.B.;  
RT "Normalization and subtraction: two approaches to facilitate gene  
RT discovery";  
RL Genome Res. 6(9):791-806(1996).  
XX  
XX UNILIB; 7277; 7277.  
XX  
CC Contact: Tuggle CK  
CC Molecular Genetics Laboratory, Department of Animal Science  
CC Iowa State University  
CC 201 Kildee Hall, Ames, IA 50011-3150, USA  
CC Tel: 5152944252  
CC Fax: 5152942401  
CC Email: cktuggle@iastate.edu  
CC The sequence contained an oligo-dT track that was present in the



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FT      /db_xref=taxon:9606"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434P065"
FT      /clone_lib="434 (synonym: htee3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX      /tissue_type="testis"
SQ      Sequence 128 BP; 20 A; 8 C; 9 G; 89 T; 2 other;

Query Match      1.3%; Score 26.8; DB 2; Length 128;
Best Local Similarity 54.2%; Pred. No. 1.8e+02;
Matches 52; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1626 TTTTGTGTCATCTGATTTCTCATTTTATTATCTGTTATCGGTCTAAAGTGCTAAATTA 1685
DB 27 TTTTGTGTCATCTGATTTCTCATTTTATTATCTGTTATCGGTCTAAAGTGCTAAATTA 86

QY 1686 CCCATTGATTTTCTGCTAGACAGATAACTTTTAA 1721
DB 87 TTTTGTGTCATCTGATTTCTCATTTTATTATCTGTTATCGGTCTAAAGTGCTAAATTA 122

RESULT 78
HSM001338/c
ID HSM001338 standard; RNA; EST; 139 BP.
XX AL037014;
XX AL037014.1
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp564G0964_r1 (from clone DKFZp564G0964)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
RN 1-139
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferpititz 18a D-82152 Martinsried, GERMANY
XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
FH source 1..139
FT /db_xref=taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp564G0964"
FT /clone_lib="564 (synonym: hfbz2). Vector pAMP1; host
FT X1-2blue; sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="brain"
XX Query Match      1.3%; Score 26.8; DB 2; Length 139;
Best Local Similarity 48.2%; Pred. No. 1.8e+02;
Matches 55; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1644 TTGTCAATTTATCTGTTATCGGTCTAAAGTGCTAAATTTACCAATTTGATTTTCTGC 1703
DB 126 TNNNTAATNNNTNGNGGTTGACNGTTTNGNTAAATTTTATTTTATTTTATTTT 67
QY 1704 TAGACAGATAACTTTTAAATTTTCAAATTTTGGCAGACACTTTTATTTTATTTT 1757
DB 66 TTTTGTGTCATCTGATTTCTCATTTTATTATCTGTTATCGGTCTAAAGTGCTAAATTA 13

RESULT 79
HSM002744
ID HSM002744 standard; RNA; EST; 147 BP.
XX AL038398;
XX AL038398.1
XX 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp566O122_s1 (from clone DKFZp566O122)
XX EST; expressed sequence tag.
XX Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX [1]
RN 1-147
RA Ottenwaelder B., Obermaier B., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferpititz 18a D-82152 Martinsried, GERMANY
XX Clone from S. Wiemann, sequenced by MediGenomix within the cDNA
CC sequencing consortium of the German Genome Project
CC No r1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX Key Location/Qualifiers
FH source 1..147
FT /db_xref=taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp566O122"
FT /clone_lib="566 (synonym: hfk2). Vector pAMP1; host
FT X1-2blue; sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="kidney"
XX Query Match      1.3%; Score 26.8; DB 2; Length 147;
Best Local Similarity 52.7%; Pred. No. 1.8e+02;
Matches 58; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1626 TTTTGTGTCATCTGATTTCTCATTTTATTATCTGTTATCGGTCTAAAGTGCTAAATTA 1685
DB 1 TTTTGTGTCATCTGATTTCTCATTTTATTATCTGTTATCGGTCTAAAGTGCTAAATTA 60
QY 1686 CCCATTGATTTTCTGCTAGACAGATAACTTTTAAATTTTCAAAATTTGG 1735
DB 61 TTTTGTGTCATCTGATTTCTCATTTTATTATCTGTTATCGGTCTAAAGTGCTAAATTA 110

RESULT 80
BF703629
ID BF703629 standard; RNA; EST; 224 BP.
XX BF703629
AC BF703629;

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XX 15-AUG-2001 (Rel. 68, Created)  
 DT 15-AUG-2001 (Rel. 68, Last updated, Version 1)  
 XX MI-P-AV1-nq1-b-01-0-UI.s1 MI-P-AV1 Sus scrofa cDNA clone  
 DE MI-P-AV1-nq1-b-01-0-UI 3', mRNA sequence.  
 DE  
 XX  
 XX EST.  
 XX  
 XX Sus scrofa (pig)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 XX  
 [1]  
 RN 1-445  
 RP MEDLINE; 97044477.  
 RA Bonaldo M.F., Lennon G., Soares M.B.;  
 RT "Normalization and subtraction: two approaches to facilitate gene  
 RL discovery";  
 RL Genome Res. 6 (9): 791-806 (1996).  
 XX  
 XX UNILIB; 7287; 7287.  
 XX  
 XX Contact: Tuggle CK  
 CC Molecular Genetics Laboratory, Department of Animal Science  
 CC Iowa State University  
 CC 201 Kildee Hall, Ames, IA 50011-3150, USA  
 CC Tel: 5152944252  
 CC Fax: 5152942401  
 CC Email: ctuggle@iastate.edu  
 CC The sequence contained an oligo-dT track that was present in the  
 CC oligonucleotide that was used to prime the synthesis of first  
 CC strand cDNA and therefore this may represent a bonafide poly A  
 CC tail. The sequence tag present in the cDNA between the NotI site  
 CC and the oligo-dT track served to verify it as a clone from the  
 CC normalized placenta library cDNA Library Preparation: M.B. Soares  
 CC Lab, University of Iowa EST sequencing: M.B. Soares Lab, University  
 CC of Iowa Clone distribution: clones will be available through  
 CC Research Genetics (www.regen.com) The following repetitive  
 CC elements were found in this cDNA sequence: 19-82,  
 CC >POLY A#simple\_repeat 113-204, >POLY A#simple\_repeat 346-445,  
 CC >POLY A#simple\_repeat  
 CC Seq primer: M13 Forward  
 CC POLY A=yes.  
 XX  
 XX Key Location/Qualifiers  
 PH source 1. .445  
 FT /db\_xref="taxon:9823"  
 FT /db\_xref="UNILIB:7287"  
 FT /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-AV1  
 FT library is normalized library derived from the MI-P-AV0  
 FT library, ultimately derived from placenta tissue. For a  
 FT detailed description of the library from which this clone  
 FT was derived, please visit our web site at  
 FT http://pigest.genome.iastate.edu/. The procedure used to  
 FT create this library has been previously described (Bonaldo  
 FT , Lennon and Soares, Genome Research 6: 791-806, 1996)  
 FT TAG\_LIB=MI-P-AV1 TAG\_TISSUE=placenta TAG\_SEQ=ATTGG"  
 FT /organism="Sus scrofa"  
 FT /strain="crossbreed"  
 FT /clones="MI-P-AV1-nq1-b-01-0-UI"  
 FT /clone\_lib="MI-P-AV1"  
 FT /lab\_host="DH10B (Life Technologies)"  
 XX  
 XX Sequence 445 BP; 243 A; 63 C; 83 G; 56 T; 0 other;  
 Query Match 1.3%; Score 26.8; DB 9; Length 445;  
 Best Local Similarity 44.1%; Pred. No. 1.4e+02;  
 Matches 112; Conservative 0; Mismatches 142; Indels 0; Gaps 0;  
 QY 1496 TATCTGTGAGACTTCATATTTCTCATCCCTTATTGCTTTTAGCAACATAGAAC 1555

Db 272 TTTTGGGGGGCTTTTGGGGGGGGTTTTTTTTTTCCCTTCCGGGGGAA 213  
 QY 1556 ATGAGTCATTTGTGTCATTAGAGTATTCTGATAAAATCTCTGAAAACTAGTAAATCAAA 1615  
 Db 212 ACCCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 153  
 QY 1616 AGGTTAATGATTTTCTGTCATTTGTCATTTTATATCTGTATCGGTCCTAAAG 1675  
 Db 152 CTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 93  
 QY 1676 TGTAAATTTACCCATTTGATTTTCTCTAGACAGATAACTTTTAAATTTTCAATTTGG 1735  
 Db 92 CCCCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 33  
 QY 1736 CAGACACTTTTTT 1749  
 Db 32 CCCCCCTTTTCTTTT 19  
 RESULT 83  
 HSM011933  
 ID HSM011933 standard; RNA; EST; 454 BP.  
 XX  
 AC AL047083;  
 XX  
 SV AL047083.1  
 XX  
 DT 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 XX  
 DE Homo sapiens mRNA; EST DKFZp586A2118\_s1 (from clone DKFZp586A2118)  
 XX  
 KW EST; expressed sequence tag.  
 XX  
 OS Homo sapiens (human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 XX  
 [1]  
 RN 1-454  
 RP Wambutt R., Heubner D., Mewes W., Gassenhuber J., Wiemann S.;  
 RA ;  
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
 XX  
 CC Clone from S. Wiemann, sequenced by AGOWA within the cDNA  
 CC sequencing consortium of the German Genome Project  
 CC No r1 sequence available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
 XX  
 PH Key Location/Qualifiers  
 FT source 1. .454  
 FT /db\_xref="taxon:9606"  
 FT /organism="Homo sapiens"  
 FT /clone="DKFZp586A2118"  
 FT /clone\_lib="586 (synonym: hute1). Vector pSport1; host  
 FT DH10B; sites NotI + SalI/WluI"  
 FT /dev\_stage="adult"  
 FT /tissue\_type="uterus"  
 XX  
 SQ Sequence 454 BP; 134 A; 87 C; 63 G; 170 T; 0 other;

Query Match 1.3%; Score 26.8; DB 2; Length 454;  
 Best Local Similarity 48.7%; Pred. No. 1.4e+02;  
 Matches 73; Conservative 0; Mismatches 77; Indels 0; Gaps 0;  
 QY 1619 TTAATGATTTTCTGTCATTTGTCATTTTATTTATCTGTTATCGGTCCTAAAGTGC 1678  
 Db 9 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 68

QY	1679	TAATTTACCAATTTGATTTTCTGCTAGACAGATAACTTTTAATTTTCAAAATTTGGCAG	1738
Db	69	TTTATTGCATAGAAATGACTGTATTAAATAATAATGCATTGTATATTTTATTGTTT	128
QY	1739	ACACTTTTTTTTTTTTTTGAAAAATCTTTC	1768
Db	129	TGTTATTATTATTTTGTGACAGAGTCTC	158
RESULT 84			
BF711270/c	standard; RNA; EST; 469 BP.		
XX	AC	AC	BF711270;
SV	XX		
XX	BF711270.1		
DT	03-JAN-2001	(Rel. 66, Created)	
DT	03-JAN-2001	(Rel. 66, Last updated, Version 1)	
XX	XX		
DE	MI-P-03-abb-c-12-1-UM.s1	MI-P-03 Sus scrofa cDNA clone	
DE	MI-P-03-abb-c-12-1-UM 3'	mRNA sequence.	
XX	XX		
XX	EST.		
XX	XX		
XX	Sus scrofa (pig)		
XX	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;	
OC	Eutheria; Cetartiodactyla;	Suina; Suidae; Sus.	
XX	[1]		
RN	1-469		
RP	MEDLINE; 97044477.		
XX	Bonaldo M.F., Lennon G., Soares M.B.;		
RA	"Normalization and subtraction: two approaches to facilitate gene		
RT	discovery";		
RL	Genome Res. 6(9):791-806(1996).		
XX	XX		
DR	UNILIB; 7285; 7285.		
XX	XX		
CC	Contact: Tuggle CK		
CC	Molecular Genetics Laboratory, Department of Animal Science		
CC	Iowa State University		
CC	201 Kildee Hall, Ames, IA 50011-3150, USA		
CC	Tel: 5152944252		
CC	Fax: 5152942401		
CC	Email: cktuggle@iastate.edu		
CC	The sequence contained an oligo-dT track that was present in the		
CC	oligonucleotide that was used to prime the synthesis of first		
CC	strand cDNA and therefore this may represent a bonafide poly A		
CC	tail. The sequence tag present in the cDNA between the NotI site		
CC	and the oligo-dT track served to verify it as a clone from the		
CC	non-normalized ovary at estrus day 12 library cDNA library		
CC	Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science		
CC	Research Center, Department of Animal Science, University of		
CC	Missouri-Columbia, 65211 Clone distribution: clones will be		
CC	available through Research Genetics (www.resgen.com) The following		
CC	repetitive elements were found in this cDNA sequence: 155-191,		
CC	>AT-rich#Low complexity		
CC	Seq primer: M13 Forward		
CC	POLYA=Yes.		
XX	XX		
XX	XX		
PH	Key	Location/Qualifiers	
PH	source		
FT	1. .469		
FT	/db xref="taxon:9823"		
FT	/db xref="UNILIB:7285"		
FT	/note="Vector: p773D-Pac (Pharmacia) with a modified		
FT	polylinker; Site_1: Not I; Site_2: EcorI; The MI-P-03		
FT	library is derived from ovary at estrus day 12. For a		
FT	detailed description of the library from which this clone		
FT	was derived, please visit our web site at		
FT	http://bigest.genome.iastate.edu/ TAG LIB=MI-P-03		

FT dT-tailed vector. The dT-tailed vector was adjusted to have  
FT about 60nt. The cDNA vector was circularized with E. coli  
FT DNA ligase after digestion of EcoRI which site is also  
FT included in vector. An RNA strand converted to a DNA strand  
FT by Okayama-Berg method. The obtained cDNA vectors were used  
FT for transformation of competent cells E. coli Top10p, by  
FT electroporation method. The cDNA libraries constructed by  
FT this method are full-length enriched cDNA library."  
FT /organism="Homo sapiens"  
FT /clone\_lib="S14K402-48-A12"  
FT /clone="S14K402-48-A12"  
FT /cell\_line="K402"  
FT /lab\_host="Top10p."  
XX

SQ Sequence 498 BP; 197 A; 81 C; 69 G; 151 T; 0 other;

Query Match 1.3%; Score 26.8; DB 2; Length 498;  
Best Local Similarity 44.1%; Pred. No. 1.4e+02;  
Matches 112; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

QY 1393 TTGTCAGCTTATCAATCAGACTGATCTAATGTAAGTATCCTTAAACAAAGC 1452  
DB 52 TTTCGACATAATCCAGTAAATATAATTTTAAAGAAATAATTTTCAATATTAGCA 111  
QY 1453 ATCTATTTCGACAGAAATGTTCTTAAATTCAGTCATTTTGATATCTGAGACATTC 1512  
DB 112 AGACAGCATGCTTCAATCAATCTGTAAGTAACTAAGAACTTAAATTTTACTG 171  
QY 1513 TATTTCATCCCTTTATGCTTTTACCAACATAGAAACCATGATCTTTTGTCAT 1572  
DB 172 CTTAATTCAAATAATATGCTAGCAATAGTAATCTGTAAGCATTAAGCTTATGCTTAAA 231  
QY 1573 TTGAGTATTCGTAAATCTCTTGAATCTGAAATCAAGAGTTAATGATTTTGG 1632  
DB 232 TTCAGTTTGTGAGGAATCTTTAAATATACAACTAAGTATGTTGATGCTATTTT 291  
QY 1633 TTCATTTCTGATTTG 1646  
DB 292 TTTCAGTTTATTTG 305

## RESULT 86

HS0004754  
ID HSM004754 standard; RNA; EST; 110 BP.  
XX AC AL040278;  
XX SV AL040278.1  
XX 12-MAR-1999 (Rel. 59, Created)  
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
XX Homo sapiens mRNA; EST DKFZp34K2413\_s1 (from clone DKFZp34K2413)  
XX EST; expressed sequence tag.

XX Homo sapiens (human)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]  
RN 1-110  
RA Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPPS, Am Klopferstritz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by BMFZ within the cDNA

CC sequencing consortium of the German Genome Project

CC This clone is also available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers  
FH source 1. 110  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone\_lib="DKFZp34K2413"  
FT /clone\_lib="434 (synonym: htes3). Vector pSport1; host  
FT DH10B; sites NotI + SalI"  
FT /dev\_stage="adult"  
FT /tissue\_type="testis"

SQ Sequence 110 BP; 11 A; 4 C; 4 G; 91 T; 0 other;

Query Match 1.3%; Score 26.6; DB 2; Length 110;  
Best Local Similarity 54.6%; Pred. No. 2e+02;  
Matches 53; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1626 TTTTGTTCATCTGATTTGTCATTTTATTTATCTGTTAAAGTCTAAATTTA 1685  
DB 1 TTTTGTTCATCTGATTTGTCATTTTATTTATCTGTTAAAGTCTAAATTTA 60

QY 1686 CCCATTTGATTTTCTGCTAGACAGATACTTTAAT 1722

DB 61 TTTTGTTCATCTGATTTGTCATTTTATTTATCTGTTAAATTTA 97

## RESULT 87

BF702532/c  
ID BF702532 standard; RNA; EST; 124 BP.

XX AC BF702532;  
XX SV BF702532.1

XX 25-DEC-2000 (Rel. 66, Created)  
DT 25-DEC-2000 (Rel. 66, Last updated, Version 1)

XX MI-P-E3-aak-d-10-1-UM s1 MI-P-E3 Sus scrofa cDNA clone

DE MI-P-E3-aak-d-10-1-UM 3', mRNA sequence.

XX EST.

XX Sus scrofa (pig)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

XX [1]  
RN 1-124  
RA MEDLINE; 97044477.  
RT Bonaldo M.F., Lemmon G., Soares M.B.;

RT "Normalization and subtraction: two approaches to facilitate gene

RL Genome Res. 6(9):791-806(1996).

XX UNILIB; 7275; 7275.

XX Contact: Tuggle CK

CC Molecular Genetics Laboratory, Department of Animal Science

CC Iowa State University

CC 201 Kildee Hall, Ames, IA 50011-3150, USA

CC Tel: 5152944252

CC Fax: 5152942401

CC Email: ktuggle@iastate.edu

CC The sequence contained an oligo-dT track that was present in the  
CC oligonucleotide that was used to prime the synthesis of first  
CC strand cDNA and therefore this may represent a bonafide poly A  
CC tail. The sequence tag present in the cDNA between the NotI site  
CC and the oligo-dT track served to verify it as a clone from the  
CC non-normalized fetus at gestational day 45 library cDNA library  
CC Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science  
CC Research Center, Department of Animal Science, University of  
CC Missouri-Columbia, 65211 Clone distribution: clones will be

CC available through Research Genetics (www.resgen.com) The following  
 CC repetitive elements were found in this cDNA sequence: 13-123,  
 CC >POLY A#Simple repeat  
 CC Seq primer: M13 Forward  
 CC POLYA=yes.

XX Key Location/Qualifiers  
 FH source  
 FT 1..124  
 FT /db\_xref="taxon:9823"  
 FT /db\_xref="UNILIB:7275"  
 FT /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 FT polylinker; Site 1: Not 1; Site 2: EcoRI; The MI-P-E3  
 FT library is derived from fetus at gestational day 45. For a  
 FT detailed description of the library from which this clone  
 FT was derived, please visit our web site at  
 FT http://pigat.genome.iastate.edu/. TAG LIB=MI-P-E3  
 FT TAG\_TISSUE=fetus at gestational day 45 TAG\_SEQ=CGCGAC"  
 FT /organism="Sus scrofa"  
 FT /strains="crossbreed"  
 FT /clone="MI-P-E3-aak-d-10-1-UM"  
 FT /clone\_lib="MI-P-E3"  
 FT /lab\_host="DH10B (Life Technologies)"  
 XX Sequence 124 BP; 110 A; 0 C; 1 G; 13 T; 0 other;

Query Match 1.3%; Score 26.6; DB 9; Length 124;  
 Best Local Similarity 52.2%; Pred. No. 2e+02; Indels 0; Gaps 0;  
 Matches 59; Conservative 0; Mismatches 54;  
 QY 1650 TTTTATTATCTGTTATCGGTCTAAAGTCTAAATTTACCCATTGATTTTCTCTAGACA 1709  
 DB 121 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 62  
 QY 1710 GATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTATTTTATTTTATTTTATTTT 1762  
 DB 61 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 9

RESULT 89  
 ID HSM010835 standard; RNA; EST; 127 BP.  
 XX AL045985;  
 XX AL045985.1  
 SV AL045985.1  
 DT 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 XX Homo sapiens mRNA; EST DKFZp4340136\_s1 (from clone DKFZp4340136)  
 XX EST; expressed sequence tag.

XX Homo sapiens (human)  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 XX [1]  
 RN Koehrer K., Beyer A., Mewes W., Gassenhuber J., Wiemann S.;  
 RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPs, Am Klopfferspitze 18a D-82152 Martinsried, GERMANY  
 XX Clone from S. Wiemann, sequenced by BMFZ within the cDNA  
 CC sequencing consortium of the German Genome Project  
 CC ri sequence also available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
 XX Key Location/Qualifiers

FH source  
 FT 1..127  
 FT /db\_xref="taxon:9606"  
 FT /organism="Homo sapiens"  
 FT /clone="DKFZp4340136"  
 FT /clone\_lib="434 (synonym: htes3). Vector pSport1; host  
 FT DH10B; sites NotI + SalI"  
 FT /dev\_stage="adult"  
 FT /tissue\_type="testis"  
 XX Sequence 127 BP; 3 A; 3 C; 6 G; 112 T; 3 other;

Query Match 1.3%; Score 26.6; DB 2; Length 127;  
 Best Local Similarity 51.3%; Pred. No. 2e+02; Indels 0; Gaps 0;  
 Matches 59; Conservative 0; Mismatches 56;  
 QY 1644 TTGTCAATTTTATCTGTTATCGGTCTAAAGTCTAAATTTACCCATTGATTTTCTGTC 1703  
 DB 1 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 60  
 QY 1704 TAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTATTTTATTTTATTTT 1758  
 DB 61 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 115

RESULT 89  
 BF703980/c  
 ID BF703980 standard; RNA; EST; 217 BP.  
 XX AC BF703980;  
 XX BF703980.1  
 DT 26-DEC-2000 (Rel. 66, Created)  
 DT 26-DEC-2000 (Rel. 66, Last updated, Version 1)  
 XX MI-P-O1-abe-h-02-1-UM.s1 MI-P-O1 Sus scrofa cDNA clone  
 DE MI-P-O1-abe-h-02-1-UM 3', mRNA sequence.  
 XX EST.

OS Sus scrofa (pig)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 XX [1]  
 RN 1-217  
 RX MEDLINE; 97044477.  
 RA Ronaldo M.F., Lennon G., Soares M.B.;  
 RT "Normalization and subtraction: two approaches to facilitate gene  
 RL discovery";  
 RL Genome Res. 6(9):791-806(1996).

XX UNILIB; 7283; 7283.  
 CC Contact: Tuggle CK  
 CC Molecular Genetics Laboratory, Department of Animal Science  
 CC Iowa State University  
 CC 201 Kildee Hall, Ames, IA 50011-3150, USA  
 CC Tel: 5152944252  
 CC Fax: 5152942401  
 CC Email: cktuggle@iastate.edu  
 CC The sequence contained an oligo-dT track that was present in the  
 CC oligonucleotide that was used to prime the synthesis of first A  
 CC strand cDNA and therefore this may represent a bonafide poly A  
 CC tail. The sequence tag present in the cDNA between the NotI site  
 CC and the oligo-dT track served to verify it as a clone from the  
 CC non-normalized ovary at estrus day 0 library cDNA library  
 CC Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science  
 CC Research Center, Department of Animal Science, University of  
 CC Missouri-Columbia, 65211 Clone distribution: clones will be  
 CC available through Research Genetics (www.resgen.com) The following  
 CC repetitive elements were found in this cDNA sequence: 1-27,

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CC >AT_rich#Low complexity
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX
FH Key Location/Qualifiers
FH source
FT 1. .217
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7283"
FT /note="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-01
FT library is derived from ovary at estrus day 0. For a
FT detailed description of the library from which this clone
FT was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. TAG LIB=MI-P-01
FT TAG_TISSUE=ovary at estrus day 0 TAG_SEQ=GACGTA"
FT /organism="Sus scrofa"
FT /strain="crossbred"
FT /clone_lib="MI-P-01"
FT /lab_host="DH10B (Life Technologies)"
XX
FH Key Location/Qualifiers
FH source
FT 1. .240
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7283"
FT /note="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-01
FT library is derived from ovary at estrus day 0. For a
FT detailed description of the library from which this clone
FT was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. TAG LIB=MI-P-01
FT TAG_TISSUE=ovary at estrus day 0 TAG_SEQ=GACGTA"
FT /organism="Sus scrofa"
FT /strain="crossbred"
FT /clone_lib="MI-P-01"
FT /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 217 BP; 105 A; 30 C; 36 G; 46 T; 0 other;

Query Match 1.3%; Score 26.6; DB 9; Length 217;
Best Local Similarity 46.9%; Pred. No. 1.8e+02;
Matches 83; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 1293 TTCTCTGTCGTGATTTTGGCCAGATGATCTGCATTTATTTGACCTTTTCTATGAT 1352
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dp 190 TTTTACCCTGCTGTTTATTTTAAACCCCATTTTATTTTGGGGGGGGT 131
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1353 TATAATCCTGTAGAAGTCACATAAAGGAGTATTTTGTGACGCTTATCAATCAGA 1412
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dp 130 TTTTCCCTCCCTCCCTTAGGAAGTTTGGGTTTGGGCCCTTTTAAACCTTT 71
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1413 CTGATCTAATGTGAATGATAGTATCCCTAAACAAAGCATCTATTTGGCAGAAA 1469
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dp 70 TTGGTTGGGATTTTATACCTTTTTCATTTTACCCCTTTTAAACCTTTTAAAAA 14
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 90
BF713193/c standard; RNA; EST; 240 BP.
XX ID BF713193
XX AC BF713193;
XX SV BF713193.1
XX 03-JAN-2001 (Rel. 66, Created)
DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX MI-P-01-adq-f-04-1-UM.B1 MI-P-01 Sus scrofa cDNA clone
DE MI-P-01-adq-f-04-1-UM 3', mRNA sequence.
XX EST.
XX Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX [1]
RN 1-240
RP MEDLINE: 97044477.
RX Ronaldo M.F., Lennon G., Soares M.B.;
RA "Normalization and subtraction: two approaches to facilitate gene
RT discovery";
RL Genome Res. 6(9):791-806(1996).
XX UNILIB: 7283; 7283.
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science

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CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: ktkuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized ovary at estrus day 0 library cDNA Library
CC Preparation: RJ Woods, JA Green, RS Prather SI42 Animal Science
CC Research Center, Department of Animal Science, University of
CC Missouri-Columbia, 65211 Clone distribution: clones will be
CC available through Research Genetics (www.resgen.com)
CC Seq primer: M13 Forward
CC POLYA=Yes.
XX Key Location/Qualifiers
FH source
FT 1. .240
FT /db_xref="taxon:9823"
FT /db_xref="UNILIB:7283"
FT /note="Vector: pT73D-Pac (Pharmacia) with a modified
FT polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-01
FT library is derived from ovary at estrus day 0. For a
FT detailed description of the library from which this clone
FT was derived, please visit our web site at
FT http://pigest.genome.iastate.edu/. TAG LIB=MI-P-01
FT TAG_TISSUE=ovary at estrus day 0 TAG_SEQ=GACGTA"
FT /organism="Sus scrofa"
FT /strain="crossbred"
FT /clone_lib="MI-P-01"
FT /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 240 BP; 110 A; 44 C; 49 G; 37 T; 0 other;

Query Match 1.3%; Score 26.6; DB 9; Length 240;
Best Local Similarity 51.2%; Pred. No. 1.7e+02;
Matches 62; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1651 TTATTATCTGTATCCGGCTAAAGTCTAATTTACCCATTTGATTTTCTGTAGACAG 1710
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dp 231 TTCATCCTTTTATTTTGAATCCCTCCCTTTTTCCTTTTTCCTGGGAT 172
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1711 ATAACCTTTTCAATTTGGCAGACACTTTTTCCTTTTTCCTTTTTCCTTTTTCCT 1770
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Dp 171 TCCTTTTATCCCGTTTAAAGTTTGGCTTTCCCTTTTTCCTTTTTCCTTTTTCCTGT 112
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1771 T 1771
Dp 111 T 111

RESULT 91
BF709445
ID BF709445 standard; RNA; EST; 300 BP.
XX AC BF709445;
XX SV BF709445.1
XX 03-JAN-2001 (Rel. 66, Created)
DT 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX MI-P-AY0-nev-a-09-0-UI.B1 MI-P-AY0 Sus scrofa cDNA clone
DE MI-P-AY0-nev-a-09-0-UI 3', mRNA sequence.
XX EST.
XX Sus scrofa (pig)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

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OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
RN 1-300
RX MEDLINE; 97044477.
RA Ronaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL discovery";
RL Genome Res. 6(9):791-806(1996).
XX
XX UNILIB; 7286; 7286.
DR
XX
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized placenta library cDNA library Preparation: M.B.
CC Soares Lab, University of Iowa EST sequencing: M.B. Soares Lab,
CC University of Iowa Clone distribution: clones will be available
CC through Research Genetics (www.resgen.com) The following repetitive
CC elements were found in this cDNA sequence: 1-99,
CC >POLY_A$Simple_repeat 221-252, >GC_rich$Low_complexity
CC Seq primer: Mi3 Forward
CC POLYA=Yes.
XX
XX Key Location/Qualifiers
FH
FH source
FH 1..300
FH /db_xref="taxon:9823"
FH /db_xref="UNILIB:7286"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-AYO
FH library is derived from placenta. For a detailed
FH description of the library from which this clone was
FH derived, please visit our web site at
FH http://pigest.genome.iastate.edu/. The procedure used to
FH create this library has been previously described (Ronaldo
FH , Lennon and Soares, Genome Research 6:791-806, 1996)
FH TAG_LIB=MI-P-AYO TAG_TISSUE=placenta TAG_SEQ=ATTGG"
FH /organism="Sus scrofa"
FH /clone="MI-P-AYO-nev-a-09-0-UI"
FH /clone_lib="MI-P-AYO"
FH /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 300 BP; 60 A; 93 C; 55 G; 92 T; 0 other;

Query Match 1.3%; Score 26.6; DB 9; Length 300;
Best Local Similarity 52.2%; Pred. No. 1.7e+02;
Matches 59; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 1690 TTGATTTTCTGTAGACAGATACCTTTAAATTTTCAATTTGGCAGACACTTTTTT 1749
Db 2 TTTTATTTTTTTTTTTTGGTCTCCCTTTTTTTTTTTTTTAAATTTTTTTTTTTTTTTT 61
QY 1750 TTTTATTTTGAATCTTCTTCAGATCTGTGCCCACTGACAGACCCCG 1802
Db 62 TTATTTTTTTTTTTTTTTTATTTATTTTATTTTCTTACCCCCCTCCCG 114

RESULT 92
BF710556/c
ID BF710556 standard; RNA; EST; 346 BP.
XX
AC BF710556;
XX

```

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SV BF710556.1
XX
XX 03-JAN-2001 (Rel. 66, Created)
XX 03-JAN-2001 (Rel. 66, Last updated, Version 1)
XX
XX MI-P-AV1-nre-e-10-0-UI-s1 MI-P-AV1 Sus scrofa cDNA clone
DE MI-P-AV1-nre-e-10-0-UI 3', mRNA sequence.
XX
XX EST.
XX
XX Sus scrofa (pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
XX
XX [1]
XX MEDLINE; 97044477.
XX Ronaldo M.F., Lennon G., Soares M.B.;
RT "Normalization and subtraction: two approaches to facilitate gene
RL discovery";
RL Genome Res. 6(9):791-806(1996).
DR
XX UNILIB; 7287; 7287.
XX
XX Contact: Tuggle CK
CC Molecular Genetics Laboratory, Department of Animal Science
CC Iowa State University
CC 201 Kildee Hall, Ames, IA 50011-3150, USA
CC Tel: 5152944252
CC Fax: 5152942401
CC Email: cktuggle@iastate.edu
CC The sequence contained an oligo-dT track that was present in the
CC oligonucleotide that was used to prime the synthesis of first
CC strand cDNA and therefore this may represent a bonafide poly A
CC tail. The sequence tag present in the cDNA between the NotI site
CC and the oligo-dT track served to verify it as a clone from the
CC non-normalized placenta library cDNA library Preparation: M.B. Soares
CC Lab, University of Iowa EST sequencing: M.B. Soares Lab, University
CC of Iowa Clone distribution: clones will be available through
CC Research Genetics (www.resgen.com) The following repetitive
CC elements were found in this cDNA sequence: 63-175,
CC >POLY_A$Simple_repeat
CC Seq primer: Mi3 Forward
CC POLYA=Yes.
XX
XX Key Location/Qualifiers
FH
FH source
FH 1..346
FH /db_xref="taxon:9823"
FH /db_xref="UNILIB:7287"
FH /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
FH polylinker; Site 1: Not I; Site 2: EcoRI; The MI-P-AV1
FH library is normalized library derived from the MI-P-AYO
FH library, ultimately derived from placenta tissue. For a
FH detailed description of the library from which this clone
FH was derived, please visit our web site at
FH http://pigest.genome.iastate.edu/. The procedure used to
FH create this library has been previously described (Ronaldo
FH , Lennon and Soares, Genome Research 6:791-806, 1996)
FH TAG_LIB=MI-P-AV1 TAG_TISSUE=placenta TAG_SEQ=ATTGG"
FH /organism="Sus scrofa"
FH /strains="crossbreed"
FH /clone="MI-P-AV1-nre-e-10-0-UI"
FH /clone_lib="MI-P-AV1"
FH /lab_host="DH10B (Life Technologies)"
XX
SQ Sequence 346 BP; 180 A; 52 C; 55 G; 59 T; 0 other;

Query Match 1.3%; Score 26.6; DB 9; Length 346;
Best Local Similarity 50.4%; Pred. No. 1.6e+02;
Matches 65; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1629 TTGTTTCATCTGATTTGTCATTTTATTATCTGTTATCGTGCTAAAGTGCTAATTTACC 1688

```







"Normalization and subtraction: two approaches to facilitate gene discovery";  
Genome Res. 6(9):791-806(1996).

UNLIB; 7281; 7281.

Contact: Tuggle CK  
Molecular Genetics Laboratory, Department of Animal Science  
Iowa State University  
201 Kildes Hall, Ames, IA 50011-3150, USA  
Tel: 5152944252  
Fax: 5152942401  
Email: cktuggle@iastate.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the non-normalized hypothalamus at estrus day 12 library cDNA library preparation: RJ Woods, JA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science, University of Missouri-Columbia, 65211 Clone distribution: clones will be available through Research Genetics (www.reagen.com) The following repetitive elements were found in this cDNA sequence: 1-39,  
>AT\_rich#Low\_complexity 40-100, >POLY\_A#simple\_repeat 371-397,  
Seq\_primer: M13 Forward  
POLYA=yes.

Key Location/Qualifiers

source 1. 446  
/db\_xref="taxon:9823"  
/db\_xref="UNLIB:7281"  
/note="vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: EcoRI; The M1-P-H3 library is derived from hypothalamus at estrus day 12. For a detailed description of the library from which this clone was derived, please visit our web site at http://pigest.genome.iastate.edu/. TAG\_LIB=M1-P-H3  
TAG\_TISSUE=hypothalamus at estrus day 12 TAG\_SEQ=GGTTAA"  
/organism="Sus scrofa"  
/strain="crossbreed"  
/clone="M1-P-H3-au-f-10-1-UM"  
/clone\_lib="M1-P-H3"  
/lab\_host="DH10B (Life Technologies)"

Sequence 446 BP; 214 A; 64 C; 60 G; 108 T; 0 other;

Query Match 1.3%; Score 26.6; DB 9; Length 446;  
Best Local Similarity 50.4%; Pred. No. 1.5e+02;  
Matches 65; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 1650 TTTTATTCTGTTATCGGTCTAAAGTCTAAATTTACCCATTGATTTTCTGCTAGACA 1709

Db 349 TTTTCTATTATTTTGGGATTTTCGGGATTTGGCTTTTTCCTGGAATTGGG 290

Qy 1710 GATACTTTTAATTTTCAAAATTTGGCAGACACTTTTTTTTTTTTCAAAATCTTTCC 1769

Db 289 AATTTAACTTGGATTTTAATTTTCCCGAATTTTAAATTTTTCGTTGGGAAACTTTTTT 230

Qy 1770 TTCCAGATC 1778

Db 229 TTTCATTC 221

RESULT 97

OS HSM004354  
ID HSM004354 standard; RNA; EST; 451 BP.

XX AC AL039878;

XX SV AL039878.1

XX 12-MAR-1999 (Rel. 59, Created)  
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
XX Homo sapiens mRNA; EST DKFZp434P2212\_s1 (from clone DKFZp434P2212)  
XX EST; expressed sequence tag.  
XX Homo sapiens (human)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.  
XX [1]  
RN 1-451  
RP Dueterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;  
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
RL M1PS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY  
XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA  
CC sequencing consortium of the German Genome Project  
CC r1 sequence also available  
CC This clone is available at the RZPD in Berlin  
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
XX Key Location/Qualifiers  
FH source 1. 451  
FT /db\_xref="taxon:9606"  
FT /organism="Homo sapiens"  
FT /clone="DKFZp434P2212"  
FT /clone\_lib="434 (synonym: htes3). Vector pSport1; host  
FT DH10B; sites NotI + SalI"  
FT /dev\_stage="adult"  
FT /tissue\_type="testis"

Sequence 451 BP; 116 A; 100 C; 69 G; 166 T; 0 other;

Query Match 1.3%; Score 26.6; DB 2; Length 451;  
Best Local Similarity 58.0%; Pred. No. 1.5e+02;  
Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1900 TTCTTGTGTGGTGCACATCTTTTAAATTTTACACCTTTTCTTAAAGAAATTCATATGCCG 1959

Db 4 TTTTCTTGTGTGTGGTGCACATCTTTTAAATTTTACACCTTTTCTTAAAGAAATTCATATGCCG 63

Qy 1960 TCTTAAAGTTTTTATACCAATA 1980

Db 64 TTGTTATTGCTATACCAATA 84

RESULT 98

ID BM856662/c standard; RNA; EST; 485 BP.

XX BM856662;

XX BM856662.1

DT 11-MAR-2002 (Rel. 71, Created)

DT 11-MAR-2002 (Rel. 71, Last updated, Version 1)

XX X-EST0140698 S14K402 Homo sapiens cDNA clone S14K402-55-E08 5', mRNA  
DE sequence.  
XX EST.

OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX [1]





GenCore version 5.1.4\_p5-4578  
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2003, 00:06:39 ; Search time 1083 Seconds  
(without alignments)  
9721.340 Million cell updates/sec

Title: US-09-877-633-2

Perfect score: 2028

Sequence: 1 caaaggacaagataataaa.....agtagacagtgatgga 2028

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6078533 seqs, 259512836 residues

Total number of hits satisfying chosen parameters: 12157066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 350 summaries

Database : GenBank-BST

1: gb\_est1.\*

2: gb\_est2.\*

3: gb\_hic.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	648.8	32.0	1014	1	AV079675 AV079675
C 2	644.6	31.8	661	1	AL574115 AL574115
C 3	633.4	31.2	1068	1	AL515908 AL515908
C 4	628.8	31.0	684	2	AW001012 W91806.X
C 5	626.6	30.9	932	2	AV726565 AV726565
C 6	601.8	29.7	664	2	BE646471 7e87d05.X
C 7	583.2	28.8	600	2	AW387914 MR4-ST011
C 8	571.2	28.2	669	2	AW964022 EST376095
C 9	551.2	27.2	563	2	AW387761 MR4-ST011
C 10	519.2	25.6	837	2	BE542593 601063983
C 11	519.2	25.6	921	1	AL562740 AL562740
C 12	503.6	24.8	659	2	AW387819 MR4-ST011
C 13	483.6	23.8	551	2	AW387869 MR4-ST011
C 14	483.6	23.8	688	1	AJ449334 AJ449334
C 15	480.6	23.7	499	2	AW387916 MR4-ST011
C 16	466.8	23.0	584	2	AW387858 MR4-ST011
C 17	456.8	22.5	460	1	AA976617 on3b10.s
C 18	450.2	22.2	778	1	AL580786 AL580786
C 19	445.2	22.0	838	1	AL524372 AL524372
C 20	442.4	21.8	614	1	AI536362 ma97f06.Y
C 21	423.4	20.9	449	1	AI083909 qf26b05.X
C 22	418.2	20.6	435	2	AW387755 MR4-ST011
C 23	418.2	20.6	429	2	AV725141 AV725141
C 24	418.2	20.6	429	2	AV729447 AV729447
C 25	418.2	20.6	429	2	AV729585 AV729585
C 26	406.6	20.0	548	2	AV747364 AV747364
C 27	405.8	20.0	1053	1	AL550164 AL550164
C 28	402.2	19.8	977	1	AL514504 AL514504
C 29	401.8	19.8	666	2	BB068522 BB068522
C 30	397.6	19.6	441	2	AW138532 UI-H-B11-





Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000).  
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001).  
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.  
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001).  
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

## FEATURES

source

Location/Qualifiers

1. .1014

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone\_lib="2210410K23"

/clone\_lib="Mus musculus stomach C57BL/6J adult"

/sex="male"

/tissue\_type="stomach"

/dev\_stage="adult"

/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5']

TGTTACCAATCGAATGGAGCGCGCGAATGGTTTTTTTTTTTTTTTTTTTT  
 T 3'; double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified pT7T3 vector.  
 RNA provided by Dr. Minoru Ko, Wayne State Univ. Library  
 constructed and normalized by Bento Soares and M. Fatima  
 Bonaldo."

BASE COUNT 266 a 238 c 252 g 256 t 2 others  
 ORIGIN

Query Match 32.0%; Score 648.8; DB 1; Length 1014;  
 Best Local Similarity 82.2%; Pred. No. 1.8e-154;  
 Matches 822; Conservative 0; Mismatches 159; Indels 19; Gaps 6;

QY 406 CCTCTCCAGACAGCCCGCAGCTTTCGCTCAACCGCAGTATCAGAGCCCTCAGACGCCA 465

Db 19 CCTCTCCGTGNCAGCCCGCCNACCTGTGTC-CAGCCAGTATCAGAGCCCTCAGACGCCA 77

QY 466 CCCAGACCCGCTGGGTGGCCCCACGACAGAAACCGCGGTTTGGCGAGCGGAGGG 525

Db 78 CTTCAACCCCGCTGT-TGGCTCTCGAAGACAGAAATGCAGCATGTGCGCAGAGTGAGGG 136

QY 526 GCTGGCAGCGATAGCAACTCTCTCTGGAAAGCTCCAGCCTAATTTGCCCCCAGCGTCGAA 585

Db 137 GCCAACAGTGACAGTAACCTCTGTTGGAAATGCCCAAGCTACTTCTGCGCCGAGTGTAAG 196

QY 586 TCCACCCCTGCTTGAAGAACTGAAGGCTCTCAGAGTACAAACCGGAAAGAGTTTGAG 645

Db 197 TCCACCCCTGCTTGGAGAACTGAAGGCTGCCCCAGAGTATACCTTAAGAGTTTCAG 256

QY 646 TGGAACTGAAAGCGGCGGTGTTTCATCATCAAGAGTACTCTGAGGACGACATCCAC 705

Db 257 TGGAACTTGAAGTGCGCGGTGTTTCATCATCAAGAGTACTCTGAGGACGACATCCAC 316

QY 706 CGCTCCATTAAGTACTCACTCTGCTGTAGCAGACGCGCAACAGCGCGCTGAGCAGC 765

Db 317 CGCTCCATCAAGTACTCACTCTGCTGTAGTACTGTAACACGCGCAACAGCGCGCTGAGCAGC 376

QY 766 GCCTCCGCTGCATGAGCAGCAAGGGGCGCGTCTACCTCTTTCAGCGTCAATGGAGT 825

Db 377 GCCTCCGCTGCATGAGCAGCAAGGGGCGCGTCTACCTCTTTCAGTGTCAATGGAGT 436

QY 826 GGGCAATTTTGTGGGTGGCGAGATGAAGTCCCCCGTGGAGTACGGCAGCAGTGGCGG 885

Db 437 GGACATTTTGTGGGTGGCGAGATGAAGTCCCCCGTGGAGTACGGCAGCAGTGGCGG 496

QY 886 GTCTGCTCTCAGCAGCAAGTGAAGGGGAAGTTTGATGTCCAGTGGAGTTTGTGTAAGGAT 945

Db 497 GTCTGCTCTCAGCAGCAAGTGAAGGGGAAGTTTGATGTGAAGTGGAGTTTGTGTAAGGAT 556

QY 946 GTACCAATAACAGCTCCGGCAGCATCAGGCTGGAGATAACGACAAACCGGTCCACA 1005

Db 557 GTGCCAACACAGCTCCGGCAGCATCAGGCTGGAGATAACGACAAACCGGTCCACA 616

QY 1006 AACTCCGGGACACCCAGAGGTGCCCTTAGAAAAAGCCAGAGTGTCTGAAAAATTATC 1065

Db 617 AACTCCGGTATACAGAGGAGTGGCCCTTAGAAAAAGCCAGAGTGTCTGAAAAATTATC 676

QY 1066 AGTTCTTACAGCAGCAACCTCCATCTTCGACGACTTTGCTCCTACGAGAGCGCCA- 1124

Db 677 GCTTCTTATAGCACACACCTCTATCTTTGACGACTTTTCTCATTTATGAGAGCGCCAG 736

QY 1125 GAGGAGGAGGAGGTGGTGGCAAGGAAAGCGCAGAGTCGAAACAAACAAATCAGGGCGAACC 1184

Db 737 GAGGAGGAGGAGGTGGTGGCAAGGAAAGCAGACATCGAAACAAACAAATCAGAAACGCC 796

QY 1185 AGTTCTTACATGTTCTAAGCTTTGACTTTGAAAAACAGTTTTAAACACGCTGTGCTGGTC 1244

Db 797 AGTTGTTGTTTGGTTAATGGTTGACTTTGAAAAACAGAGTTTAAAGCTGTATGCTGGTG 856

QY 1245 AGCT-----CCAGTGTCTCGTCCGCTCGGGGTTGAGTGTGCATCTTTGCGCT 1293

Db 857 CTGCTCCGAGTCAGCTCCAGTGTGCTGCTCGTGGCGGGTTGATTGTGATCTTTATCT 916

QY 1294 TTCTTGTGCTGTGATTTTGGCCAGATGGATCTGCATTTATTTGACTTTTTTCTATGTATT 1353

Db 917 TTCTAG----TTCATTTTGGCAGATGGATCTGCATTCATTGTGA-TTTTCTATGTATT 971

QY 1354 ATATCTCTGTAGAGTCACTAATAAAGGAGTATTTTTTTT 1393

Db 972 ATAATATTGTAGAACTCACTAATAAAGGAGTATTTTGT 1011

RESULT 2  
 AL574115/c  
 LOCUS

DEFINITION AL574115 LTI\_NFL006.PL2 Homo sapiens cDNA clone CS0D1040YK06.3  
 prime, mRNA sequence.

ACCESSION AL574115

VERSION AL574115.1 GI:12934008

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 661)

AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polyes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr).

Location/Qualifiers

1. .661

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="CS0D1040YK06"

/clone\_lib="LTI\_NFL006.PL2"

/tissue\_type="placenta"

/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA



was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT	119 a	179 c	178 g	181 t	4 others
ORIGIN					
Query Match	31.8%; Score 644.6; DB 1; Length 661;				
Best Local Similarity	99.1%; Pred. No. 1.9e-153;				
Matches 655; Conservative	2; Mismatches 3; Indels 1; Gaps 1;				
Qy	527	CTGGCAGCGATAGCAACTCTCTGGAAAGCTCCAGAGCTTAATCTTGCCCCAGCGTCGAAT	586		
Db	661	CTGGCAGCGATAGCAAVTCTCTGGAAAGCTCCAGAGCTTAATCTTGCCCCAGCGTCGAAT	602		
Qy	587	CCNACCCGCTCTTGAANAATGAAGCTGCTCACAGCTACAAACCCGAAAGAGTTTCAGT	646		
Db	601	CCCACCCGCTCTTGAANAATGAAGCTGCTCACAGCTACAAACCCGAAAGAGTTTCAGT	542		
Qy	647	GGAAATCTGAAAAGCGGCTGTTCATCATCAAGAGCTACTCTGAGGACGACATCCACC	706		
Db	541	GGAAATCTGAAAAGCGGCTGTTCATCATCAAGAGCTACTCTGAGGACGACATCCACC	482		
Qy	707	GCTCCATTAAGTACTCCATCTGGTGTAGCACAGACGCGCAACGCGCTGCACAGCG	766		
Db	481	GCTCCATTAAGTACTCCATCTGGTGTAGCACAGACGCGCAACGCGCTGCACAGCG	422		
Qy	767	CTTTCGCTGCATGAGCAGCAAGGGGCCCTGTACTGTCTTTACGCGTCAATGGGAGTG	826		
Db	421	CTTTCGCTGCATGAGCAGCAAGGGGCCCTGTACTGTCTTTACGCGTCAATGGGAGTG	362		
Qy	827	GGCAATTTTGTGGGGTGGCGGAGATGAAGTCCCGGTGAGCTACGGCACAGTGCAGGGG	886		
Db	361	GGCAATTTTGTGGGGTGGCGGAGATGAAGTCCCGGTGAGCTACGGCACAGTGCAGGGG	302		
Qy	887	TCTGGTCTCAGGACAAGTGGAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGATG	946		
Db	301	TCTGGTCTCAGACAGATGGGAAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGATG	242		
Qy	947	TACCCAATAACAGCTCCGGCACATCAGGCTGGAGAAATACGCAACAACACCGGTACAA	1006		
Db	241	TACCCAATAACAGCTCCGGCACATCAGGCTGGAGAAATACGCAACAACACCGGTACAA	182		
Qy	1007	ACTCCCGGACACCCAGAGGTGCCCTTAGAAAAAGCCAAAGCAAGTGTGAAATTTATCA	1066		
Db	181	ACTCCCGGACACCCAGAGGTGCCCTTAGAAAAAGCCAAAGCAAGTGTGAAATTTATCA	122		
Qy	1067	GTTCCTACAGCACACACCTTCATCTTCGACGACTTTGTCTACTACGAGAGCGCCA-G	1125		
Db	121	GTNCCTACAGCACACACCTTCATCTTCGACGACTTTGTCTACTACGAGAGCGCCAAGG	62		
Qy	1126	AGGAGGAGGAGTGGTGGCGCAAGGAAACGGCAGAGTGCMAAACAATAGAGGCGGAACCA	1185		
Db	61	AGGAGGAGGAGTGGTGGCGCAAGGAAACGGCAGAGTGCMAAACAATAGAGGCGGAACCA	2		
Qy	1186	G 1186			
Db	1	G 1			
RESULT 3					
AL515908/c					
LOCUS					
DEFINITION	AL515908 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA001YB18 3				
ACCESSION	prime, mRNA sequence.				
AL515908					
VERSION	AL515908.1 GI:12779401				
KEYWORDS	EST.				

SOURCE ORGANISM human. Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1068)  
AUTHORS Li M.B., Gruber C., Jessee J. and Polayes D.  
TITLE full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 382 a 217 c 187 g 275 t 7 others

ORIGIN

Query Match 31.2%; Score 633.4; DB 1; Length 1068;

Best Local Similarity 98.0%; Pred. No. 1.5e-150;

Matches 646; Conservative 5; Mismatches 6; Indels 2; Gaps 1;

Qy	1370	CACATAAAGGAGTATTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAT	1429		
Db	1068	CACATAAAGGAGTATTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAT	1011		
Qy	1430	GTAAGTATCTTAAACAAAGCATCTATTTGGCAGAAATGTGTCTTAATTCAGTC	1489		
Db	1010	GTGAGTATCTTAAACAAAGCATCTATTTGGCAGAAATGTGTCTTAATTCAGTC	951		
Qy	1490	ATTGATATCTGTGAGCTTCATATTTCTCATCCCTTTATTTGCTTTTAGCAACATAA	1549		
Db	950	ATTGATATCTGTGAGCTTCATATTTCTCATCCCTTTATTTGCTTTTAGCAACATAA	891		
Qy	1550	GAACCATGAGTCATTTGTCATTTAGAGTATTTCTGATAAAATCTCTGAAATACCTGAA	1609		
Db	890	GAACCATGAGTCATTTGTCATTTAGAGTATTTCTGATAAAATCTCTGAAATACCTGAA	831		
Qy	1610	ATCAAAAGGTTAATGATTTTTTGTTCATTCGTATTTGTCTATTTATTTATCTGTATCGGT	1669		
Db	830	ATCAAAAGGTTAATGATTTTTTGTTCATTCGTATTTGTCTATTTATTTATCTGTATCGGT	771		
Qy	1670	CTAAAGTGTATTTTACCCATTTGATTTTCTGTAGACAGATACTTTTAATTTTCAA	1729		
Db	770	CTAAAGTGTATTTTACCCATTTGATTTTCTGTAGACAGATACTTTTAATTTTCAA	711		
Qy	1730	ATTGGCAGACACTTTTTTTTTTTTTCGAAATCTTTCTCCAGATCTGTGTGCCACT	1789		
Db	710	ATTGGCAGACACTTTTTTTTTTTTTCGAAATCTTTCTCCAGATCTGTGTGCCACT	651		
Qy	1790	GAACAGCCACCGCTCCCTCAGCTGTCTGTGTGTCGGAATGGGCTGGATGTGTGGGGCAT	1849		
Db	650	GAACAGCCACCGCTCCCTCAGCTGTCTGTGTGTCGGAATGGGCTGGATGTGTGGGGCAT	591		
Qy	1850	GATGTGTGAGGAACATGGAGGTGCTTTAGGCTGTGTTTCTGAGGTCGGGATCTTTGTTG	1909		





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QY 1220 CAGTTTAAACACGCTGTGCTTGGTTCAGCTCCAGTGTGTCGTCCCGTGGGGGTTGAGTG 1279
Db 184 CAGTTTAAACACGCTGTGCTTGGTTCAGCTCCAGTGTGTCGTCCCGTGGGGGTTGAGTG 125
QY 1280 TTGCATCTTTGCCCTTCTTCTGTCGTTGATTTTGGCCAGATCGATCTGCATTTATTTGTAC 1339
Db 124 TTGCATCTTTGCCCTTCTTCTGTCGTTGATTTTGGCCAGATCGATCTGCATTTATTTGTAC 65
QY 1340 TTTTCTATGTATTATTAATCTCTAGAGAGTCACTAATAAAGGAGTATTTTTTTT 1393
Db 64 TTTTCTATGTATTATTAATCTCTAGAGAGTCACTAATAAAGGAGTATTTTTTTT 11

RESULT 7
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LOCUS AW387914 600 bp mRNA linear EST 04-FEB-2000
DEFINITION MR4-ST0119-071099-010-F01 ST0119 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW387914
VERSION AW387914.1 GI:6892573
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 600)
HCCP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-ST0119-071099-010-F01&t3=1999-10-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 581.
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/db_xref="taxon:9606"
/clone_lib="ST0119"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 124 a 169 c 151 g 156 t
ORIGIN
Query Match 28.8%; Score 583.2; DB 2; Length 600;
Best Local Similarity 99.3%; Pred. No. 7.8e-138;
Matches 596; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 676 ATCAAGAGCTACTCTGAGGACGACATCCACCGCTCCATTAACTACTCCATCTGGTGATGC 735
Db 600 ATCAAGAGCTACTCTGAGGACGACATCCACCGCTCCATTAACTACTCCATCTGGTGATGC 541
QY 736 ACAGAGCAGCGCAACAGCGCTGGACAGCGCTTCGCTGCATGACGAGGAGGCGCC 795
Db 540 ACAGAGCAGCGCATCAAGCGCTGGACAGCGCTTCGCTGCATGACGAGGAGGCGCC 481
QY 796 GTCTACCTGCTCTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGGTGGCCGAGATCAAG 855
Db 480 GTCTACCTGCTCTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGGTGGCCGAGATCAAG 421
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QY 856 TCCCCCTGGACTACGGCACACAGTGGCCGGGGTCTGGTCTCAGGACAAAGTGAAGGGGAAG 915
Db 420 TCCCCCTGGACTACGGCACACAGTGGCCGGGGTCTGGTCTCAGGACAAAGTGAAGGGGAAG 361
QY 916 TTGTATCTCCAGTGGATTTTGTAAAGATGTACCCCAATACCAAGCTCCGGCACATCAGG 975
Db 360 TTGTATCTCCAGTGGATTTTGTAAAGATGTACCCCAATACCAAGCTCCGGCACATCAGG 301
QY 976 CTGAGAGATTAACGACAAACACCGGTCAACAACTCCCGGGACACCCAGGAGGTGCCCTTA 1035
Db 300 CTGAGAGATTAACGACAAACACCGGTCAACAACTCCCGGGACACCCAGGAGGTGCCCTTA 241
QY 1036 GAAAAAGCCAAAGTGTGCTGAAATTTATCAGTTCTTACAGACACAACTCCATCTTC 1095
Db 240 GAAAAAGCCAAAGTGTGCTGAAATTTATCAGTTCTTACAGACACAACTCCATCTTC 181
QY 1096 GACGACTTCTCTACTACGAGAACGCCA-CAGGAGGAGGAGGTGGTCCGCAAGAACGG 1154
Db 180 GACGACTTCTCTACTACGAGAACGCCA-CAGGAGGAGGAGGTGGTCCGCAAGAACGG 121
QY 1155 CAGAGTCGAAACAAACAAATGAGGGCGAACAGTTTCTTACATGTTCTAAAGCTTTGACTTT 1214
Db 120 CAGAGTCGAAACAAACAAATGAGGGCGAACAGTTTCTTACATGTTCTTAAAGCTTTGACTTT 61
QY 1215 GAAAAAGTTTAAACACGTTGCTTGGTTCAGCTCCAGTGTGTCCTCCGTCGGGGGTT 1274
Db 60 GAAAAAGTTTAAACACGTTGCTTGGTTCAGCTCCAGTGTGTCCTCCGTCGGGGGTT 1

RESULT 8
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LOCUS AW964022 669 bp mRNA linear EST 01-JUN-2000
DEFINITION EST376095 MAGE resequences, MAGH Homo sapiens cDNA, mRNA sequence.
ACCESSION AW964022
VERSION AW964022.1 GI:8153858
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 669)
Hegde, P., Qi, R., Aherthy, K., Dharap, S., Gaspar, R., Gay, C., Holt,
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 196
Seq primer: Reverse.
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/note="Vector: pBluescriptSKm"
BASE COUNT 175 a 107 c 135 g 252 t
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Best Local Similarity 97.4%; Pred. No. 1e-134;
Matches 591; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 1396 TCAGCTTATCAATCAGACTGATTAATGTGAATGTAAAGTATCTTAAAAACAAGATC 1455
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QY 1456 TATTTTGGCAGAAATGTGTTCTTAAATTCAGTCATTTGATATTTCTGTGAGACTTCATAT 1515
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QY 1516 TTCTCATCCCTTATTGCTTTTATAGCAACATAAGAAACCATGAGTCATTTTGTCAATTTA 1575
Db 121 TTCTCATCCCTTATTGCTTTTATAGCAACATAAGAAACCATGAGTCATTTTGTCAATTTA 180
QY 1576 GAGTATTCGATAAAATCTCTTTGAAATAACTGAAATCAAAAGGTTAAATGATTTTGTTC 1635
Db 181 GAGTATTCGATAAAATCTCTTTGAAATAACTGAAATCAAAAGGTTAAATGATTTTGTTC 240
QY 1636 ATTCGATTTGTCATTTTATTTATCTGTTATCGTCTAAAGTCTCTAATTTACCATTGAT 1695
Db 241 ATTCGATTTGTCATTTTATTTATCTGTTATCGTCTAAAGTCTCTAATTTACCATTGAT 300
QY 1696 TTTTCTGTGAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACAC-TTTTTTTTTTTT 1754
Db 301 TTTTCTGTGAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACCTTTTTTTTTTTT 360
QY 1755 TTTGAAATCTTTTCCCTTCAGATCTGTTCGCCACTGAACAGCCACCCGTCCTCACTGTC 1814
Db 361 TTTGAAATCTTTTCCCTTCAGATCTGTTCGCCACTGAACAGCCACCCGTCCTCACTGTC 420
QY 1815 CTGTGTCGATTTGGCTGGATGTTGGGCGATGATGTGGAGGAACTGGAAGGTGC 1874
Db 421 CTGTGTCGATTTGGCTGGATGTTGGGCGATGATGTGGAGGAACTGGAAGGTGC 480
QY 1875 TTTAGTCTGTTTCAGGTCGGGCACTTTGTTGTTTCACATCTTTTAAATTTTACA 1934
Db 481 TTTAGTCTGTTTCAGGTCGGGCACTTTGTTGTTTCACATCTTTTAAATTTTACA 540
QY 1935 CTTTTTCTTAAAGATTTCTAATGCCGCTTAAAGTTTATACCAATAATGCTGAGCTTTTAA 1994
Db 541 CTTGTTTCAAGATTTCTAATGCAAGTTTATAGTTGTTATACCAATAATGCTGAGCTTTTAA 600
QY 1995 GTGTAGG 2001
Db 601 ATGGTGG 607

RESULT 9
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LOCUS MR4-ST0118-041099-010-C01 ST0118 Homo sapiens cDNA, mRNA sequence.
DEFINITION MR4-ST0118-041099-010-C01 ST0118 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW387761
VERSION AW387761.1 GI:6892420
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 563)
HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC0&t2=MR4-ST0118-041099-010-C01&t3=1999-10-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 523.
Location/Qualifiers
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/organism="Homo sapiens"
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/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No.196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 116 a 161 c 139 g 147 t
ORIGIN
Query Match 27.2%; Score 551; DB 2; Length 563;
Best Local Similarity 99.8%; Pred. No. 1.2e-129;
Matches 562; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 713 TTAAGTACTCCATCTGCTAGCAGAGCAGCGCAACAGCGCTGACAGCGCTTCC 772
Db 563 TTAAGTACTCCATCTGCTAGCAGAGCAGCGCAACAGCGCTGACAGCGCTTCC 504
QY 773 GCTGATGAGCAGCAAGGGGCGGCTCTACCTGCTCTTTCAGCGTCAATGGAGTGGGCAAT 832
Db 503 GCTGATGAGCAGCAAGGGGCGGCTCTACCTGCTCTTTCAGCGTCAATGGAGTGGGCAAT 444
QY 833 TTTGTGGGTGGCCGAGATGAAGTCCCGCTGGAGTACGGCACAGTGCCTGGGTCTGCT 892
Db 443 TTTGTGGGTGGCCGAGATGAAGTCCCGCTGGAGTACGGCACAGTGCCTGGGTCTGCT 384
QY 893 CTCAGACAGTGGGAAGGGAGTTTGTATCCAGTGGATTTTCTTAAGGATGTACCA 952
Db 383 CTCAGACAGTGGGAAGGGAGTTTGTATCCAGTGGATTTTCTTAAGGATGTACCA 324
QY 953 ATAACAGCTCCGGCACATCAGGCTGGAGATAACGACAAACCGGTCAAAATCTCC 1012
Db 333 ATAACAGCTCCGGCACATCAGGCTGGAGATAACGACAAACCGGTCAAAATCTCC 264
QY 1013 GGGACACCCAGAGTGCCTTTAGAAAAGCCAAAGTGTCTGAAAATTTATCAGTTCT 1072
Db 263 GGGACACCCAGAGTGCCTTTAGAAAAGCCAAAGTGTCTGAAAATTTATCAGTTCT 204
QY 1073 ACAAGCACACACCTCCATCTTCGAGCACTTTGCTCCTACGAGAGCGCA-GAGGAGG 1131
Db 203 ACAAGCACACACCTCCATCTTCGAGCACTTTGCTCCTACGAGAGCGCAAGGAGG 144
QY 1132 AGGAGTGTGTGGCAAGGAAACGGCAGAGTCGAAACAAACATGAGGGCGAAACAGTTTCT 1191
Db 143 AGGAGTGTGTGGCAAGGAAACGGCAGAGTCGAAACAAACATGAGGGCGAAACAGTTTCT 84
QY 1192 TACATGTTTCTAACGTTTGAATTTGAAAACAGTTTAAAACACGTTGCTTGGTCAAGTCCA 1251
Db 83 TACATGTTTCTAACGTTTGAATTTGAAAACAGTTTAAAACACGTTGCTTGGTCAAGTCCA 24
QY 1252 GTGTGTCGTCCTCCGTCGGGGGTT 1274
Db 23 GTGTGTCGTCCTCCGTCGGGGGTT 1
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LOCUS 601063983F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450261 5',
DEFINITION mRNA sequence.
ACCESSION BE542593
VERSION BE542593.1 GI:9771238
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 837)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
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JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-i@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution by: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LL48428 row: f column: 22  
High quality sequence stop: 631.  
Location/Qualifiers

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source

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/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."  
193 a 231 c 252 g 161 t

BASE COUNT 193 a 231 c 252 g 161 t  
ORIGIN

Query Match 25.6%; Score 519.2; DB 2; Length 837;  
Best Local Similarity 92.8%; Pred. No. 1.7e-121;  
Matches 655; Conservative 0; Mismatches 38; Indels 13; Gaps 10;

QY 577 AGCGTGAATCCCAACCCCGCTTGAAGAACTGAAGGCTGTACACGCTACAACCCGAAA 636  
DB 1 AGCGTGAATCCCAACCCCGCTTGAAGAACTGAAGGCTGTACACGCTACAACCCGAAA 60  
QY 637 GAGTTTGAAGTGAATCTGAAGCGGCGTGTGTTCAT-CATCAAGAGTACTCTGAGGA 695  
DB 61 GAG-TTGAAGTGAATCTGAAGCGGCGTGTGTTCATCATCAAGAGTACTCTGAGGA 119  
QY 696 CGACATCCCGC-CTCCATTAGTACTCTCCATCTGGTGTAGCAGACGCGGCAACAGC 754  
DB 120 CGACATCCCGCCTCCATTAGTACTCTCCATCTGGTGTAGCAGACGCGGCAACAGC 179  
QY 755 GCCTGGACAGCGCTCCCGC-TGCATGAGCAGCAAGGCGCGCTCTACCTGCTCTCAGC 813  
DB 180 GCCTGGACAGCGCTCCCGCGTGCATGAGCAGCAAGGCGCGCTCTACCTGCTCTCAGC 239  
QY 814 GTCATGGAGTGGGCATTTTGTGGGTGGCCGAGATGAAGTCCCGCTGGACTACGGC 873  
DB 240 GTCATGGAGTGGGCA-TTTTGTGGGTGGCCGAGATGAAGTCCCGCTGGACTACGGC 297  
QY 874 ACCAGTCCCGGCTGTGCTCAGGACAGTGGAGGGGAGTTTGATGCTCCAGTGCATT 933  
DB 298 ACCAGTCCCGGCTGTGCTCAGGACAGTGGAGGGGAGTTTGATGCTCCAGTGGCA-T 356  
QY 934 TTTGTTAAGGATGATCCCAATTAACAGCTCCGGCAGATCAGGCTGGAGATAACGACAAC 993  
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DB 417 AAAACCGGTCAAACTCCCGGACACCCAGGAGTGCCTTTAGAAAAGCAAGCAAGTG 476  
QY 1054 CTGAATATATCAGTTCTACAGCAGACACCTCCATCTTCGACGACTTTGCTCACTAC 1113  
DB 477 CTGAATATATCAGTTCTACAGCAGACACCTCCATCTTCGACGACTTTGCTCACTAC 536  
QY 1114 GAGAAGCGCCAG--AGGAGGAGGAGTGGTGGCGCAAGCAAGCAAGTGCAGAACCAACA 1171  
DB 537 GAGAAGCGCCAGGAGGAGGAGGAGTGGTGGCG-AGGACCGGAGAGTGCAGAACATAC 595  
QY 1172 ATGAGGCGCAACCAAGTTCTTACATGTTCTTAAGTGTTCATTTGATCTTTGAAACAGTTTAAACA 1231  
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Db 596 AATGGGGGAACAGTCTCTTACATGTTCTTAACGTTGACTTT--GAACACGTTAAACCC 652  
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RESULT 11  
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DEFINITION AL562740 LTI\_NFL003\_NBC3 Homo sapiens cDNA clone CS0DC020104 3  
Prime, mRNA sequence.

ACCESSION AL562740

VERSION AL562740.1 GI:12911458

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 921)

AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

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/lab\_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 323 a 196 c 170 g 222 t 10 others

ORIGIN

Query Match 25.6%; Score 519; DB 1; Length 921;  
Best Local Similarity 98.5%; Pred. No. 1.9e-121;  
Matches 517; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1504 GAGACTTCATATTTCTCATCCCTTTATGCTTTTACCAACATAAGAAACCATGATCA 1563  
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QY 1564 TTTTGTCTATTAGAGATTTCTGATAAATCTTGAATACTGAAATCAAAGGTTAAT 1623  
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QY 1624 GATTTTGTCTATTAGAGATTTCTGATAAATCTTGAATACTGAAATCAAAGGTTAAT 1683  
DB 801 GATTTTGTCTATTAGAGATTTCTGATAAATCTTGAATACTGAAATCAAAGGTTAAT 742

QY 1684 TACCCATTTGATTTTCTGCTAGACAGATAAATTTTAAATTTTCAAATTTGGCAGACACT 1743  
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QY 1744 TTTTGTCTATTAGAGATTTCTGATAAATCTTGAATACTGAAATCAAAGGTTAAT 1803  
DB 681 TTTTGTCTATTAGAGATTTCTGATAAATCTTGAATACTGAAATCAAAGGTTAAT 622

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QY 1804 CCTCATCTCTCTGCTCCGATGGGCTGGATGGTGTGGGGGCATGATGTGGAGGAA 1863
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QY 1864 CTGGAGGTGCTTTAGTCTGCTCAGGCTCGGGCAATCTCTGTTGTTGGACATCTTTT 1923
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QY 1924 TAAATTTTACACCTTTTCTTAAGAATTTCTAATGCCGCTTTAAGTTTATACCAATAATG 1983
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Db 501 TAAATTTTACACCTTTTCTTAAGAATTTCTAATGCCGCTTTAAGTKTTATACCAATAATG 442
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QY 1984 CTGAGCTTTAAGTGTAGGATCTGCTAGTACAGACAGATGTGATGGA 2028
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Db 441 CTGAGCTTTAAGTGTAGGATCTGCTAGTACAGACAGATGTGATGGA 397
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LOCUS MR4-ST0118-021299-021-a06 ST0118 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW387819
ACCESSION AW387819
VERSION AW387819.1 GI:6892478
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 659)
HCGP http://www.ludwig.org.br/ORESTES.
AUTHORS The FAPESP/LICR Human Cancer Genome Project
TITLE Unpublished (1999)
JOURNAL Contact: Simpson A.J.G.
COMMENT Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-ST0118-021299-021-a06&t3=1999-12-02&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 658.
Location/Qualifiers
1..659
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0118"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site: 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 178 a 175 c 179 g 127 t
ORIGIN

Query Match 24.8%; Score 503.6; DB 2; Length 659;
Best Local Similarity 95.8%; Pred. No. 1.5e-117;
Matches 571; Conservative 0; Mismatches 19; Indels 6; Gaps 5;

QY 559 CAGCCTAATTTCTGCCCCAGCGTCGAATCCACCCCGTCTCTGAAACCTGAAGGCTGCT 618
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Db 22 CAGCCTAATTTCTG--CCACGCGTCGAATCCACCCCGTCTCTGAAACTGAAGCTGCTC 79
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QY 619 CACAGCTACACCCGAAAGATTTGAGTGAATCTGAAAA-GGGGCGTGTGTTCATCAT 677
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Db 80 ACGACTACACCCGAAAGAGTTTGAATGGATCTGAAAAGCGGGCGTGTGTTTCATCAT 139
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QY 678 CAA-GAGCTACTCTGAGGACGACATCCACCGCTCCATTAAAGTACTCCATCTGGGTATAGCA 736
|||||
Db 140 CAATGAGCTACTCTGAGGACGACATCCACCGCTCCATTAAAGTACTCCATCTGGGTATAGCA 199
|||||
QY 737 CAGAGCAGGCAACAAAGCGCTGGACAGCGCTTCGCTGCGATGAGCAGCAGAGGGGGCCG 796
|||||
Db 200 CAGAGCAGGCAACAAAGCGCTGGACAGCGCTTCGCTGCGATGAGCAGCAGAGGGGGCCG 259
|||||
QY 797 TCTACTGCTCTTTCAGCGTCAATGGGAGTGGGCATTTTGTGGGCTGGCCGAGAGTGAAGT 856
|||||
Db 260 TCTACTGCTCTTTCAGCGTCAATGGGAGTGGGCATTTTGTGGGCTGGCCGAGAGTGAAGT 319
|||||
QY 857 CCCCCGTGGACTACGGCACCAAGTCCC-GGGGTCTGGTCTCAGGACAAAGTGGAGGGGAAG 915
|||||
Db 320 CCCCCGTGGACTACGGCACCAAGTCCC-GGGGTCTGGTCTCAGGACAAAGTGGAGGGGAAG 379
|||||
QY 916 TTTGATGTCAGTGGATTTTGTAAAGATGTACCC--ATAACCAAGCTCCGCCACATCAG 974
|||||
Db 380 TTTGATGTCAGTGGATTTTGTAAAGATGTACCCAAATAACCAAGCTCCGCCACATCAG 439
|||||
QY 975 GCTGGAGAATAACGACACAAACACCGGTCAAACTCCCGGGACACCCAGGAGGTGCCCTT 1034
|||||
Db 440 GCTGGAGAATAACGACACAAACACCGGTCAAACTCCCGGGACACCCAGGAGGTGCCCTT 499
|||||
QY 1035 AGAAAAAGCCAAGCAAGTGTCTGAAAATTTATCAGTTCTTCAACAGCACACACCTCCATCTT 1094
|||||
Db 500 AGAAAAAGCCAAGCAAGTGTCTGAAAATTTATCAGTTCTTCAACAGCACACACCTCCATCTT 559
|||||
QY 1095 CGACGACTTTGCTCACTACGAGAGCGCCAGAGGAGGAGGAGTGTGGCGCAAGGA 1150
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Db 560 CGACGACTTTGCTCACTACGAGAGCGCCAGAGGAGGAGGAGTGTGGCGCAAGGA 615
|||||

RESULT 13
AW387869/c 551 bp mRNA linear EST 04-FEB-2000
LOCUS MR4-ST0118-151299-023-d10 ST0118 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW387869
ACCESSION AW387869
VERSION AW387869.1 GI:6892528
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 551)
HCGP http://www.ludwig.org.br/ORESTES.
AUTHORS The FAPESP/LICR Human Cancer Genome Project
TITLE Unpublished (1999)
JOURNAL Contact: Simpson A.J.G.
COMMENT Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-ST0118-151299-023-d10&t3=1999-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 484.
Location/Qualifiers
1..551
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0118"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
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derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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BASE COUNT      111 a   155 c   143 g   142 t
ORIGIN

Query Match      23.8%; Score 483.6; DB 2; Length 551;
Best Local Similarity 96.8%; Pred. No. 1.7e-112;
Matches 536; Conservative 0; Mismatches 14; Indels 4; Gaps 4;

QY 716 AGTACTCCATCTGGTGTAGCACAGACACGGCAACAGCGCCTGGACAGCGCCTTCGGCT 775
DB 551 AGTACTCCATCTGGT-TAGCACAGACACGGCAACAGCGCCTGG-CAGCGCCTTCGGCT 494
QY 776 GCATGACACAGAGGGCCGCTTACCTGCTTTCACGGTCAATGGGAGTGGGCAATTTT 835
DB 493 GCATGACACAGAGGGCCGCTTACCTGCTTTCACGGTCAATGGGAGTGGGCAATTTT 434
QY 836 GTGGGGTGGCGGAGATGAAGTCCCGCTGGACTACGGCACAGTGGCGGGGTCTGGTCTC 895
DB 433 CTGGGGTGGCGGAGATGAAG-CCCGCTGGACTACGGCACAGTGGCGGGGTCTGGTCTC 375
QY 896 AGGACAAGTGGAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGGATGTACCCAAATA 955
DB 374 AGGACAAGTGGAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGGATGTACCCCAATA 315
QY 956 ACCAGCTCCCGGCACATCAGGCTGGAGATTAACGACAAACCGGTCCACAACTCCCGGG 1015
DB 314 ACCAGCTCCCGGCACATCAGGCTGGAGATTAACGACAAACCGGTCCACAACTCCCGGG 255
QY 1016 ACACCCAGGAGTGGCCCTTAGAAAAAGCCAAAGCAAGTGTGTAATAATTATCAGTTCTTACA 1075
DB 254 ACACCCAGGAGTGGCCCTTAGAAAAAGCCAAAGCAAGTGTGTAATAATTATCAGTTCTTACA 195
QY 1076 AGCACAACTCCATCTTCGACACTTTGCTCTACTAGAGAAAGCGCCA-GAGGAGAGG 1134
DB 194 AGCACAACTCCATCTTCGACACTTTGCTCTACTAGAGAAAGCGCCAGGAGGAGG 135
QY 1135 AGTGGTGGCCAGGACGCGAGTGCAGAAACAAACAACTAGGCGCAACAGTTTCTTAC 1194
DB 134 AGTGGTGGCCAGGACGCGAGTGCAGAAACAAACAACTAGGCGCAACAGTTTCTTAC 75
QY 1195 ATGTTCTAACGTTTGACTTTTGAACACAGTTTAAACACAGTGTGCTTGGTCAGCTCCAGTG 1254
DB 74 ATGTTCTAACGTTTGACTTTTGAACACAGTTTAAACACAGTGTGCTTGGTCAGCTCCAGTG 15
QY 1255 TGTGCTCCCGTGG 1268
DB 14 TGTGCTCCCGTGG 1

RESULT 14
AJ449334      688 bp   mRNA   linear   EST 19-APR-2002
LOCUS
DEFINITION   AJ449334 riken1 Gallus gallus cDNA clone 21k24r1, mRNA sequence.
ACCESSION   AJ449334
VERSION      AJ449334.1 GI:20216555
KEYWORDS     EST,
SOURCE       chicken.
ORGANISM     Gallus gallus
              Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
              Phasianinae; Gallus.
              1 (bases 1 to 688).
REFERENCE    Buerstedde,J.M.
AUTHORS      Gallus gallus bursal lymphocyte EST
TITLE        Unpublished (2002)
JOURNAL      Contact: Buerstedde JM
COMMENT      Cellular Immunology
              Heinrich-Pette-Institute
              Martinistr. 52, 20251 Hamburg, Germany
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Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.  
Location/Qualifiers  
1. .688  
/organism="Gallus gallus"  
/db\_xref="taxon:9031"  
/clone="21k24r1"  
/clone\_lib="riken1"  
/cell\_type="bursal lymphocyte"  
/dev\_stage="2-3 weeks old"  
/note="CB inbred strain"

BASE COUNT 206 a 156 c 157 g 169 t  
ORIGIN

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Query Match      23.8%; Score 483.6; DB 1; Length 688;
Best Local Similarity 82.5%; Pred. No. 1.8e-112;
Matches 566; Conservative 0; Mismatches 119; Indels 1; Gaps 1;

QY 440 CGCAGTATCAGAGCCCTCAGCAGCCACCCAGACCCGCTGGGTGGCCCAACGCAAGAA 499
DB 2 CACAGTATCAGAGCCCTCAACAGCCACCCCAAATCGCTGGATTGCTTCGCAACAGAA 61
QY 500 ACCGGCGCTTTGGGACAGAGCGAGGGGCTGGCAGCGATAGCAACTCTCTGGAAACGTCC 559
DB 62 ATGACGCTTTTGGCCAAAGTGGAGGAACCTGGTAATGACAGCAATTGAGTGGCAGTACCC 121
QY 560 AGCTTAATTCTGCCCCAGCGTCGAATCCACCCCGCTCTTGAATAAAGTGAAGGCTGCTC 619
DB 122 AGCTTAACCTGTTCCAAAGTGGTGGTCCCATCTCTGTTCTTGAATAAAGTGAAGGCTGCTC 181
QY 620 ACAGCTACACCCGAAAGAGTTTGAAGTGAATCTGAAGCGGGCTGTGTTTCATCATCA 679
DB 182 ACAGCTATTAATCTCAAGATTTTGAATGAACCTTAAATAATGACGCTGTGTTTCAATAA 241
QY 680 AGAGCTACTCTGAGGACGACATCCACCGTCCATTAAGTACTCCATCTGGTGTAGCACAG 739
DB 242 AGAGCTATTCTGAGGATGATATTCATCGTTCATTAAGTATTCTATTGTTGTTAGTACG 301
QY 740 AGCAGGCAACAAAGCCCTGGACAGCGCTTCGCTGTCATAGCAGCAAGGCGCCGCTCT 799
DB 302 AGCATGGCAACAAACGCTGGACAGTGTCTTCCGTCCATGAATAGCAAGGCTCCGCTCT 361
QY 800 ACCTGCTCTTCAGCTCAATGGAGTGGGCAATTTTGGGGTGGCGGAGATCAAGTCCC 859
DB 362 ACTTGTCTTTCAGTGTCAATGGCAGTGGACACTTCTGTGGAGTTGACAGATGAATATCAC 421
QY 860 CCGTGGACTACGGCACACAGTCCCGGGTCTGGTCTCAGGACAAAGTGGAGGGAAAGTTTG 919
DB 422 CTGTGGACTATGGCACCAAGTGGCAGTGTGCTGTCTCAGGACAAAGTGGAGGGAAAGTTTG 481
QY 920 ATGTCAGTGGATTTTGTAAAGGATGTACCCAAATTAACCAAGTCCGGCAGCATCAGGCTGG 979
DB 482 ATGTCAGTGGATTTTGTAAAGGATGTGCCCAACCAACAGCTCCGACACATCAGGCTGG 541
QY 980 AGAATAACGACAAACCCGCTCACAACCT-CCGGGACACCCAGGAGTGGCTCTAGAA 1038
DB 542 AGAACAATGACAAACAAACCTGTTTACAAACTCCCGGTGACACAGAGGAGTGCCTCTAGAA 601
QY 1039 AAAGCCAAGCAAGTGTGTAATAATTATCAGTTCCTACAGCACACAACTCCATCTTCGAC 1098
DB 602 AAAGCAAAACAGTGTGTAATAATTATGCTACTTACAGCACACGACCTCCATCTTTGAT 661
QY 1099 GACTTTGCTCCTACGAGAGCGCCA 1124
DB 662 GACTTTTCTCATTATGAAAAGCGCCA 687

RESULT 15
AW387916/c
LOCUS
DEFINITION   MR4-ST0119-071099-010-F04 ST0119 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW387916
VERSION      AW387916.1 GI:6892575
KEYWORDS     EST.
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SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 499)  
TITLE HCGP <http://www.ludwig.org.br/ORESTES>.  
JOURNAL The FAPESP/LICR Human Cancer Genome Project  
COMMENT Unpublished (1999)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-ST0119-071059-010-F04&t3=1999-10-07&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence stop: 465.  
FEATURES  
1. 499  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="ST0119"  
/dev\_stage="Adult"  
/note="Organ: stomach; Vector: puc18; Site:1: SmaI;  
Site:2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 103 a 144 c 118 g 134 t  
ORIGIN  
Query Match 23.7%; Score 480.6; DB 2; Length 499;  
Best Local Similarity 99.0%; Pred. No. 9.8e-112;  
Matches 494; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 777 CATGACGACGAGGGCCCGTCTACTGCTCTTACGCTCAATGGAGTGGGCAATTTTG 836  
Db 499 CATGACGACGAGGGCCCGTCTACTGCTCTTACGCTCAATGGAGTGGGCAATTTTG 440  
QY 837 TGGGGTGGCGGAGTCAATCCCGTGGACTACGGCACGAGTCCGGGTCTGGTCTCA 896  
Db 439 TGGGGTGGCGGAGTCAATCCCGTGGACTACGGCACGAGTCCGGGTCTGGTCTCA 380  
QY 897 GCACAAAGTGGAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGATGTACCCCAATAA 956  
Db 379 GCACAAAGTGGAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGATGTACCCCAATAA 320  
QY 957 CCAGTCTCCGACATCAGGCTGGAGAAATACGACAAACACCGGTCAAAATCCCGGGA 1016  
Db 319 CCAGTCTCCGACATCAGGCTGGAGAAATACGACAAACACCGGTCAAAATCCCGGGA 260  
QY 1017 CACCCAGGAGGTGCCCTTAGAAAACCGAAGCAGTGTGAAAATATCAGTTCCTACAA 1076  
Db 259 CACCCAGGAGGTGCCCTTAGAAAACCGAAGCAGTGTGAAAATATCAGTTCCTACAA 200  
QY 1077 GCACAAACCTCCATCTTCGAGACTTTGCTACTACGAGNAGCGCA - GAGGAGGAGGA 1135  
Db 199 GCACAAACCTCCATCTTCGAGACTTTGCTACTACGAGNAGCGCGAGGAGGAGGA 140  
QY 1136 GGTGGTGCAGGAAGGACGGCAGAGTGCAGAACCAACAAATGAGGCGCAACCAAGTTTCTTACA 1195  
Db 139 GGTGGTGCAGGAAGGACGGCAGAGTGCAGAACCAACAAATGAGGCGCAACCAAGTTTCTTACA 80  
QY 1196 TGTCTTAAAGCTTTGATTTGAAACAGTTTAAACACGTTGGTTCAGTCCAGTGT 1255  
Db 79 TGTCTTAAAGCTTTGATTTGAAACAGTTTAAACACGTTGTGAATGTCAGTCCAGTGT 20

QY 1256 GTGTCCTCGTCCGGGGGTT 1274  
Db 19 GTGTCCTCGTCCGGGGGTT 1  
RESULT 16  
AW387858/c 584 bp mRNA linear EST 04-FEB-2000  
LOCUS MR4-ST0118-151299-023-b10 ST0118 Homo sapiens cDNA, mRNA sequence.  
DEFINITION AW387858  
ACCESSION AW387858  
VERSION AW387858.1 GI:6892517  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 584)  
TITLE HCGP <http://www.ludwig.org.br/ORESTES>.  
JOURNAL The FAPESP/LICR Human Cancer Genome Project  
COMMENT Unpublished (1999)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-ST0118-151299-023-b10&t3=1999-12-15&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence stop: 496.  
FEATURES  
1. 584  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="ST0118"  
/dev\_stage="Adult"  
/note="Organ: stomach; Vector: puc18; Site:1: SmaI;  
Site:2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 121 a 161 c 151 g 151 t  
ORIGIN

Query Match 23.0%; Score 466.8; DB 2; Length 584;  
Best Local Similarity 92.9%; Pred. No. 3.3e-108;  
Matches 522; Conservative 0; Mismatches 37; Indels 3; Gaps 3;  
QY 707 GCTCCATTAAAGTACTCCATCTGTTAGCAGACGACGCAAGCGCTTGGACAGCG 766  
Db 561 GCACCTCCATTAACTCTCTGTTAGCAGTCAAGCGCACAAAGCGCTTGGAAAGCGC 502  
QY 767 CCTTCGGTGCATGACGACGAAGGGGCCGCTCTACTGCTTTCAGCGTCAATGGAGTG 826  
Db 501 CTTCCCTGGCATGACGACAA - GGGCGCGTCTACTGCTCTTACGCGTCAATGGAGTG 443  
QY 827 GGCATTTTGTGGGTGGCCGAGATGAAGTCCCGTGGACTACGCGCACAGTCCGGGG 886  
Db 442 GGCATTTTGTGGGTGGCCGAGATGAAGTCCCGTGGACTACGCGCACAGTCCGGGG 383  
QY 887 TCTGCTCTCAGGACAAAGTGGAGGGGAAGTTTGATGTCTCAGTGGATTTTGTAAAGGATG 946  
Db 382 TCTGCTCTCAGGACAAAGTGGAGGGGAAGTTTGATGTCTCAGTGGATTTTGTAAAGGATG 323  
QY 947 TACCAATAACCAAGTCCCGGACATCAGCGTGGAGAAATAACGACAAACCAACCGGTCAAA 1006  
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Db 322 TACCCATACAGCTCCGGCAGCATCAGGCTGGAGAAATACGACAAACACCGGTACAG 263
QY 1007 ACTCCCGGACACCCAGGAGTCCCTTAGAAAAAGCC-AAGCAAGTGTGAAAAATTATC 1065
Db 262 ACTCCCGGACACCCAGGAGTCCCTTAGAAAAAGCCAAAGCAAGTGTGAAAAATTATC 203
QY 1066 AGTTCCTACAAGCACACAACTCCATCTTCGACGACTTTCCTCACTACGAGAAAGCGCCA- 1124
Db 202 AGTTCCTACAAGCACACAACTCCATCTTCGACGACTTTCCTCACTACGAGAAAGCGCCAG 143
QY 1125 GAGGAGGAGAGTGTGGCCAGGACGCGACAGTGTGAAACAAACAACTAGGCGGCAACC 1184
Db 142 GAGGAGGAGAGTGTGGCCAGGACGCGACAGTGTGAAACAAACAACTAGGCGGCAACC 83
QY 1185 AGTTCCTACATGTTCTAAAGTGTGACTTTGAAAAAGAGTTTAAACACAGTGTGCTGGTC 1244
Db 82 AGTTCCTACATGTTCTAAAGTGTGACTTTGAAAAAGAGTTTAAACACAGTGTGCTGGTC 23
QY 1245 AGTCCAGTGTGTCGCCGTG 1266
Db 22 AGTCCAGTGTGTCGCTCGC 1

RESULT 17
AA976117 460 bp mRNA linear EST 22-MAY-1998
LOCUS on33b10.s1 NCI_CGAP_Lus Homo sapiens cDNA clone IMAGE:1558459 3',
DEFINITION mRNA sequence.
ACCESSION AA976117
VERSION AA976117.1 GI:3151909
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 460)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@imail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 439.
Location/Qualifiers
1. 460
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1558459"
/clone_lib="NCI_CGAP_Lus"
/tissue_type="carcinoid"
/lab_host="DHI08"
/notes="Organ: lung; Vector: p7T3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p7T3 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
```

BASE COUNT 123 a 78 c 79 g 180 t

Query Match 22.5%; Score 456.8; DB 1; Length 460;  
Best Local Similarity 99.6%; Pred. No. 1.1e-105;

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Matches 458; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1402 TATCAATCAGACTGATCTAATGTGAAATCTAAGTATCTCTTAAACAAAGCATCTATTTT 1461
Db 1 TATCAATCAGACTGATCTAATGTGAAATCTAAGTATCTCTTAAACAAAGCATCTATTTT 60
QY 1462 GGAGAGAAATGTGTTCTTAAATTCAGTCAATTTGATATTTCTGGTGAAGACTTCATATTTCTCA 1521
Db 61 GGAGAGAAATGTGTTCTTAAATTCAGTCAATTTGATATTTCTGGTGAAGACTTCATATTTCTCA 120
QY 1522 TCCCTTTATTTGCTTTTATAGCAACATAGAAACCATGAGTCAATTTTGTGATTTAGAGTAT 1581
Db 121 TCCCTTTATTTGCTTTTATAGCAACATAGAAACCATGAGTCAATTTTGTGATTTAGAGTAT 180
QY 1582 TCTGATAAAATCTCTTGAATACTGAAATCAAAAGGTTAATGATTTTGTTCATTTCTG 1641
Db 181 TCTGATAAAATCTCTTGAATACTGAAATCAAAAGGTTAATGATTTTGTTCATTTCTG 240
QY 1642 ATTTGTCAATTTATTTATCTGTTATCGGTCTAAAGTCTTAATTTACCATTTGATTTTCT 1701
Db 241 ATTTGTCAATTTATTTATCTGTTATCGGTCTAAAGTCTTAATTTACCATTTGATTTTCT 300
QY 1702 GCTAGACAGATACTTTTAAATTTTCAAAATTTGCGACAGACATTTTGTGTTTGTGAAA 1761
Db 301 GCTAGACAGATACTTTTAAATTTTCAAAATTTGCGACAGACATTTTGTGTTTGTGAAA 360
QY 1762 ATCTTTCCCTCCAGATCTGTGTCCTCACTGAACAGCACCCGTCCTCACTGTCTGTGT 1821
Db 361 ATCTTTCCCTCCAGATCTGTGTCCTCACTGAACAGCACCCGTCCTCACTGTCTGTGT 420
QY 1822 CCGATTGGGCTGGATCGTGTGCGGCGATGATGTGTGGAGG 1861
Db 421 CCGATTGGGCTGGATCGTGTGCGGCGATGATGTGTGGAGG 460

RESULT 18
AL580786 778 bp mRNA linear EST 16-FEB-2001
LOCUS AL580786 LTI_NFL008.TC2 Homo sapiens cDNA clone CS0DJ014YN09 5
DEFINITION prime, mRNA sequence.
ACCESSION AL580786
VERSION AL580786.1 GI:12947147
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 778)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 778
/organism="Homo sapiens"
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/notes="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : liang@lifetech.com URL :
http://fulllength.invitrogen.com
```



Waterston, R. and Wilson, R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)  
Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
This read is a RESEQUENCE of a previously sequenced mouse clone  
This read has been verified (found to hit its original self in the  
correct orientation)  
MGI:209275  
Seq primer: -40RP from Gibco  
High quality sequence stop: 463  
POLYA=No.

FEATURES  
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1. .614  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone\_lib="IMAGE:318659"  
/dev\_stage="19.5 dpc total fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/notes="Vector: pT73D (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5',  
TGTTACCAATCTCAAGTGGGCGCGCATTTTTTTTTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M. Fatima Bonaldo. RNA was kindly provided by  
Dr. Minoru Ko (Wayne State University)."

BASE COUNT 169 a 136 c 163 g 144 t 2 others  
ORIGIN  
Query Match 21.8%; Score 442.4; DB 1; Length 614;  
Best Local Similarity 86.3%; Pred. No. 5.5e-102;  
Matches 499; Conservative 0; Mismatches 78; Indels 1; Gaps 1;  
QY 667 GTGTTTCATCATCAAGAGCTACTCTGAGAGCAGATCCACGCTCCATTAAGTACTCCATC 726  
DB 2 GTGTTTCATCATCAAGAGCTATTCTGAGGAGCAGATCCACGCTCCATCAAGTACTCCATC 61  
QY 727 TGGTGTAGCAGACGACGCGCAACAGCGCTGACAGCGCTTCCGCTGCATGAGCAGC 786  
DB 62 TGGTGTAGTACTGAACACGCGCAACAGCGCTGACAGCGCTTCCGCTCCATGAGCAGC 121  
QY 787 AAGGGGCGCGTCTACCTGCTCTTCCAGGCTCAATGGGAGTGGGCAATTTTGTGGGTGGCC 846  
DB 122 AAGGGGCGCTGTTATCTCTCTTCCAGTGTCAATGGGAGTGGACATTTCTGTGGGTGGCA 181  
QY 847 GAGATGAAGTCCCGCGTGGACTACGGCACCAGTGC CGGGTCTGGTCTCAGGCAAGTGG 906  
DB 182 GAGATGAAGTCCCGTGGACTACGGCACCAGCGCTGGGCTGTGCTCAGGCAAGTGG 241  
QY 907 AAGGGGAAGTTTGAATGTCAGTGGATTTTGTAAAGATGTACCAATACAGCTCCGG 966  
DB 242 AAGGGGAAGTTTGAATGTTGAATGTTGTTTGTGAAGATGTGCCCAACACAGCTCGG 301  
QY 967 CACATCAGGCTGAGAAATACGACAAACACCGGTCAAACTCCCGGGACACCCAGGAG 1026  
DB 302 CACATCAGACTGGAGATACGACAAACACCTGTCAAACTCCCGTGTATACAGGAG 361  
QY 1027 GTGCCCTTAGAAAAAGCAAAGCAAGTCTGAAATTTATCATGTTCTTCAAGCACAAC 1086  
DB 362 GTGCCCTTAGAAAAAGCAAACAAAGTCTGAAGATTATCGCTTCTTATAGCACAAC 421  
QY 1087 TCCATCTTCACGACTTTGCTCTACTAGCAGACGGCCA-GAGGAGGAGGAGTGGTGGC 1145

Db 422 TCTATCTTTGACGACTTTTCTCATTTAGAGAGCCGAGGAGGAGGAGTGGTGGT 481  
QY 1146 AAGGACGCGCAGAGTTCGAAACAAACATAGGCGGCAACCACTTTCTTACATGTTCTTAACG 1205  
DB 482 AAGGAAAGACAGAAATCGAAACAAACATAGAACACCAAGTCTTTGTTTGGTTAATGGT 541  
QY 1206 TTTGACTTTTGAAACAGTTTTAAACACAGCTGTGCTGTGT 1243  
DB 542 TGACTNTGAAACAGAGTTNTAAAGCTGTATGCTGTGT 579

RESULT 21  
AI083909/c  
LOCUS  
DEFINITION  
qf26b05.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:1751121 3'  
similar to TR:04503 004503 SEQUENCE OF BAC F21M12 FROM ARABIDOPSIS  
THALIANA CHROMOSOME 1, COMPLETE SEQUENCE. ; mRNA sequence.  
ACCESSION AI083909.1 GI:3422332  
VERSION AI083909.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 449)  
REFERENCE  
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/Brn25), Tumor Gene Index  
JOURNAL Unpublished (1998)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@email.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/hbrp/image/image.html  
Insert length: 1946 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 418.  
FEATURES  
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1. .449  
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/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:1751121"  
/clone\_lib="NCI CGAP Brn25"  
/issue\_type="anaplastic oligodendroglioma"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5',  
TGTTACCAATCTCAAGTGGGCGCGCATTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT73 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT 120 a 106 c 100 g 123 t  
ORIGIN  
Query Match 20.9%; Score 423.4; DB 1; Length 449;  
Best Local Similarity 99.3%; Pred. No. 3.4e-97;  
Matches 446; Conservative 0; Mismatches 1; Indels 2; Gaps 2;  
QY 960 GCTCCGCGCATCAGGCTGGAGAAATACGACAAACCGGTCAAACTCCCGGGACAC 1019  
DB 449 GCTCCGCGCATCAGGCTGGAGAAATACGACAAACCGGTCAAACTCCCGGGACAC 390

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QY 1020 CCAGGAGTGCCCTTAGAAAAAGCCAGCAAGTGTCTGAAATTTATCAGTTCTCTACAAGCA 1079
Db 389 CCAGGAGTGCCCTTAGAAAAAGCCAGCAAGTGTCTGAAATTTATCAGTTCTCTACAAGCA 330
QY 1080 CACAACCTCCATCTTCGACGACTTTGCTCCTACAGAGAGCCCA-GAGGAGGAGAGGT 1138
Db 329 CACAACCTCCATCTTCGACGACTTTGCTCCTACAGAGAGCCCA-GAGGAGGAGAGAGGT 270
QY 1139 GGTGGCAGGAGCAAGCGCAGAGTCGAAACAAACAAATGAGGGCGAACCAGTTCTTACATGT 1198
Db 269 GGTGGCAGGAGCAAGCGCAGAGTCGAAACAAACAAATGAGGGCGAACCAGTTCTTACATGT 210
QY 1199 TCTACAGTTTGACTTTGAAAAACAGTTTAAACACAGTGTCTGCTGGTCAGCTCCAGTGTGTC 1258
Db 209 TCTACAGTTTGACTTTGAAAAACAGTTTAAACACAGTGTCTGCTGGTCAGCTCCAGTGTGTC 150
QY 1259 GTCCCGTGGGGGGTGTGAGTGTGCACTTTCCTTCTGCTGTTGATTTTGGCCACA 1318
Db 149 GTCCCGTGGGGGGTGTGAGTGTGCACTTTCCTTCTGCTGTTGATTTTGGCCACA 90
QY 1319 TGGATCTGCATTTATTTGTACTTTTCTATGTATTATAATCCTGTAGAAAGTCACTAATAA 1378
Db 89 TGGATCTGCATTTATTTGTACTTTTCTATGTATTATAATCCTGTAGAAAGTCACTAATAA 30
QY 1379 AGGAGTATTTTGTGTCAGCTTATCAA 1407
Db 29 AGGAGTATTTGTCAGCTTATCAA 2

RESULT 22
AW387755/c
LOCUS MR4-ST0118-041099-010-A06 ST0118 Homo sapiens cDNA, mRNA sequence.
DEFINITION MR4-ST0118-041099-010-A06 ST0118 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW387755
VERSION AW387755.1 GI:6892414
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC0&t2=MR4-ST0118-041099-010-A06&t3=1999-10-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 434.
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="ST0118"
            /dev_stage="Adult"
            /note="Organ: stomach; Vector: puc18; Site: 1: SmaI;
            Site: 2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the pUC 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
        90 a 121 c 104 g 120 t
BASE COUNT
ORIGIN
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Query Match 20.6%; Score 418.2; DB 2; Length 435;
Best Local Similarity 99.1%; Pred. No. 7.2e-96;
Matches 431; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 841 GTGGCCGAGATGAAGTCCCGTGGACTACGCGACAGTGCCTGGGGTCTGGTCTCAGGAC 900
Db 435 GTGGCCGAGATGAAGTCCCGTGGACTACGCGACAGTGCCTGGGGTCTGGTCTCAGGAC 376
QY 901 AAGTGGAAAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGGATGTACCCCAATACCAG 960
Db 375 AAGTGGAAAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGGATGTACCCCAATACCAG 316
QY 961 CTCGGGCAATCAGCTGGAGATAAACAACAACAAACCGGTCAAACTCCGGGACACC 1020
Db 315 CTCAGCAATCAGCTGGAGATAAACAACAACAAACCGGTCAAACTCCGGGACACC 256
QY 1021 CAGGAGGTGCCCTTAGAAAAAGCCAAAGTGTCTGAAAAATTTATCAGTTCTTACATGTT 1080
Db 255 CAGGAGGTGCCCTTAGAAAAAGCCCTAGCAAGTGTCTGAAAAATTTATCAGTTCTTACATGTT 196
QY 1081 ACAACCTCCATCTTCGACGACTTTTCTCTACCTACGAGAAAGCGCCA-GAGGAGGAGGAGTG 1139
Db 195 ACAACCTCCATCTTCGACGACTTTTCTCTACCTACGAGAAAGCGCCAGGAGGAGGAGTG 136
QY 1140 GTGCCAAAGGAACGGCAGAGTCGAAACAAACAATCAGGCGGCAACAGTTTCTTACATGTT 1199
Db 135 GTGCCAAAGGAACGGCAGAGTCGAAACAAACAATCAGGCGGCAACAGTTTCTTACATGTT 76
QY 1200 CTAACGTTTGACTTTCAAAACAGTTTAAACACAGTCTGGTCAGTCCAGTCTGTCG 1259
Db 75 CTAACGTTTGACTTTGAAACAGTTTAAACACAGTCTGGTCAGTCCAGTCTGTCG 16
QY 1260 TCCCGTGGCGGGGTT 1274
Db 15 TCCCGTGGCGGGGTT 1

RESULT 23
AW725141
LOCUS AV725141 HTC Homo sapiens cDNA clone HTCMH07 5', mRNA sequence.
DEFINITION AV725141 HTC Homo sapiens cDNA clone HTCMH07 5', mRNA sequence.
ACCESSION AV725141
VERSION AV725141.1 GI:10830231
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 429)
AUTHORS Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu
S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA HTC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
    Location/Qualifiers
        1..429
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="HTCMH07"
            /clone_lib="HTC"
            /tissue_type="Hypothalamus"
            /dev_stage="Adult"
            /lab_host="SOLR"
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/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      125 a   59 c   57 g   188 t
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Query Match      20.6%; Score 418; DB 2; Length 429;
Best Local Similarity 99.8%; Pred. No. 8.1e-96;
Matches 429; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1329 TTTATTGTACTTTTCTATGTATTATAAATCCTGTAGAAGTCACATAAAGGAGTATTT 1388
DB 1 TTTATTGTACTTTTCTATGTATTATAAATCCTGTAGAAGTCACATAAAGGAGTATTT 59
QY 1389 TTTTGTGACGCTTATCAATCAGACTGATCTAATGTGAAGTCACTAATAAGGAGTATTT 1448
DB 60 TTTTGTGACGCTTATCAATCAGACTGATCTAATGTGAAGTCACTAATAAGGAGTATTT 119
QY 1449 AAGCATCTATTTGGCAGAAATTTGTCTTAAATTCAGTCATTTGATATCTGTGAGAC 1508
DB 120 AAGCATCTATTTGGCAGAAATTTGTCTTAAATTCAGTCATTTGATATCTGTGAGAC 179
QY 1509 TCCATATTTCTCATCCCTTTATTTAGCAAACTAAGAAACCATGAGTCATTTTG 1568
DB 180 TCCATATTTCTCATCCCTTTATTTAGCAAACTAAGAAACCATGAGTCATTTTG 239
QY 1569 TCATTTAGAGTATTTCTGATAAAATCTCTTGAAATCTGAAATCAAAAGGTTAATGATTT 1628
DB 240 TCATTTAGAGTATTTCTGATAAAATCTCTTGAAATCTGAAATCAAAAGGTTAATGATTT 299
QY 1629 TTTGTCATTTCTGATTTGTCATTTATATCTGTTATCGGTCTAAAGTGCTAATTTACCC 1688
DB 300 TTTGTCATTTCTGATTTGTCATTTATATCTGTTATCGGTCTAAAGTGCTAATTTACCC 359
QY 1689 ATTGTATTTTCTGTAGACAGATAACTTTTAAATTTTCAAAATTTGCGACACTTTTTT 1748
DB 360 ATTGTATTTTCTGTAGACAGATAACTTTTAAATTTTCAAAATTTGCGACACTTTTTT 419
QY 1749 TTTTATTTTG 1758
DB 420 TTTTATTTTG 429
RESULT 24
AV729447 AV729447 HTC Homo sapiens cDNA clone HTCAMP05 5', mRNA sequence.
LOCUS AV729447
DEFINITION AV729447 HTC Homo sapiens cDNA clone HTCAMP05 5', mRNA sequence.
ACCESSION AV729447
VERSION AV729447.1 GI:10838868
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 429)
AUTHORS Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu
S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Shen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA HTC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
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1. .429
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HTCAMP05"
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/clone_lib="HTC"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      125 a   59 c   57 g   188 t
ORIGIN
Query Match      20.6%; Score 418; DB 2; Length 429;
Best Local Similarity 99.8%; Pred. No. 8.1e-96;
Matches 429; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1329 TTTATTGTACTTTTCTATGTATTATAAATCCTGTAGAAGTCACATAAAGGAGTATTT 1388
DB 1 TTTATTGTACTTTTCTATGTATTATAAATCCTGTAGAAGTCACATAAAGGAGTATTT 59
QY 1389 TTTTGTGACGCTTATCAATCAGACTGATCTAATGTGAAGTCACTAATAAGGAGTATTT 1448
DB 60 TTTTGTGACGCTTATCAATCAGACTGATCTAATGTGAAGTCACTAATAAGGAGTATTT 119
QY 1449 AAGCATCTATTTGGCAGAAATTTGTCTTAAATTCAGTCATTTGATATCTGTGAGAC 1508
DB 120 AAGCATCTATTTGGCAGAAATTTGTCTTAAATTCAGTCATTTGATATCTGTGAGAC 179
QY 1509 TCCATATTTCTCATCCCTTTATTTAGCAAACTAAGAAACCATGAGTCATTTTG 1568
DB 180 TCCATATTTCTCATCCCTTTATTTAGCAAACTAAGAAACCATGAGTCATTTTG 239
QY 1569 TCATTTAGAGTATTTCTGATAAAATCTCTTGAAATCTGAAATCAAAAGGTTAATGATTT 1628
DB 240 TCATTTAGAGTATTTCTGATAAAATCTCTTGAAATCTGAAATCAAAAGGTTAATGATTT 299
QY 1629 TTTGTCATTTCTGATTTGTCATTTATATCTGTTATCGGTCTAAAGTGCTAATTTACCC 1688
DB 300 TTTGTCATTTCTGATTTGTCATTTATATCTGTTATCGGTCTAAAGTGCTAATTTACCC 359
QY 1689 ATTGTATTTTCTGTAGACAGATAACTTTTAAATTTTCAAAATTTGCGACACTTTTTT 1748
DB 360 ATTGTATTTTCTGTAGACAGATAACTTTTAAATTTTCAAAATTTGCGACACTTTTTT 419
QY 1749 TTTTATTTTG 1758
DB 420 TTTTATTTTG 429
RESULT 25
AV729585 AV729585 HTC Homo sapiens cDNA clone HTCANC06 5', mRNA sequence.
LOCUS AV729585
DEFINITION AV729585 HTC Homo sapiens cDNA clone HTCANC06 5', mRNA sequence.
ACCESSION AV729585
VERSION AV729585.1 GI:10839006
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 429)
AUTHORS Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu
S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Shen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA HTC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HTCCAN06"
/clone_lib="HTC"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 125 a 59 c 57 g 188 t
ORIGIN
Query Match 20.6%; Score 418; DB 2; Length 429;
Best Local Similarity 99.8%; Pred. No. 8.1e-96;
Matches 429; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1329 TTTATTGTACCTTTTCTATGATTAATATCTCTGTAGAGTCACTAATAAGGAGTATT 1388
Db 1 TTTATTGTACCTTTTCTATGATTAATATCTCTGTAGAGTCACTAATAAGGAGTATT 59
QY 1389 TTTTGTGTCAGCTTATCAATCAGACTGATCTAATGTGAATGTAAAGTATCCTTAAACAA 1448
Db 60 TTTTGTGTCAGCTTATCAATCAGACTGATCTAATGTGAATGTAAAGTATCCTTAAACAA 119
QY 1449 AAGCATCTATTTGGCAGAAATGTCTTCTAAATTCAGTCAATTCGATATTCGTGAGAC 1508
Db 120 AAGCATCTATTTGGCAGAAATGTCTTCTAAATTCAGTCAATTCGATATTCGTGAGAC 179
QY 1509 TTTCATATTTCTATCCCTTTATTTGCTTTTGTAGCAACATAGAAACCTAGTCAATTTG 1568
Db 180 TTTCATATTTCTATCCCTTTATTTGCTTTTGTAGCAACATAGAAACCTAGTCAATTTG 239
QY 1569 TCATTTAGAGTATTCGATAAATCTCTGAAATCTGAAATCAAAAGCTTAATCATTT 1628
Db 240 TCATTTAGAGTATTCGATAAATCTCTGAAATCTGAAATCAAAAGCTTAATCATTT 299
QY 1629 TTGTGTCATTCGATTTGTCATTTATTTATCTGTTATCGTCTPAAAGTCTAATTTACCC 1688
Db 300 TTGTGTCATTCGATTTGTCATTTATTTATCTGTTATCGTCTPAAAGTCTAATTTACCC 359
QY 1689 ATTGATTTTTCGTAGACAGATACTTTTAAATTTTCAAAATTCGACAGACTTTT 1748
Db 360 ATTGATTTTTCGTAGACAGATACTTTTAAATTTTCAAAATTCGACAGACTTTT 419
QY 1749 TTTTTTTGTG 1758
Db 420 TTTTTTTGTG 429
RESULT 26
AV747364 548 bp mRNA linear EST 19-OCT-2000
LOCUS AV747364 NPC Homo sapiens cDNA clone NPCKE10 5', mRNA sequence.
DEFINITION AV747364
ACCESSION AV747364.1 GI:10905212
VERSION EST.
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 548)
AUTHORS Song,H., Peng,Y., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N.,
Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu
,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Ye,M., Zhang,Q.,
Han,Z., Chen,Z., Hu,R. and Chen,J.
Homo sapiens NPC library cDNA clones
Unpublished (2000)
Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
```

```
Email: mbshi@sm.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
FEATURES
source
1..548
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NPCKE10"
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/dev_stage="Adult"
/lab_host="SOLR"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
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BASE COUNT 149 a 118 c 127 g 143 t 11 others
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Query Match 20.0%; Score 406.6; DB 2; Length 548;
Best Local Similarity 91.0%; Pred. No. 6.9e-93;
Matches 483; Conservative 0; Mismatches 42; Indels 6; Gaps 5;
QY 915 GTTTCATGTCCTCAGTCGATTTTGTAAAGATGTACCAATACCAGCTCCGGCAGATCAG 974
Db 1 GGTTCATGTCCTCAGTCGAGGCTTTNACAGGCGACACCTCTCAGCAAGGCCCGGGATGAACAG 60
QY 975 GCTCGAGAAATACGACAAACACCGGTCAAACTCCCGGGACACCCAGAGAGTGCCCTT 1034
Db 61 CTTGAGAAATACGACAAACACCGGTCAAACTCCCGGGACACCCAGAGAGTGCCCTT 120
QY 1035 AGAAAAAGCAAGCAAGTCTGAAAATTTATCAGTTCTTCAACAGCACAACTCCATCTT 1094
Db 121 AGAAAAAGCAAGCAAGTCTGAAAATTTATCAGTTCTTCAACAGCACAACTCCATCTT 180
QY 1095 CGACGACTTTGCTACTAGGAGAGGCGCA-CAGGAGGAGGAGTGTCGCAAGAACG 1153
Db 181 CGACGACTTTGCTACTAGGAGAGGCGCA-CAGGAGGAGGAGTGTCGCAAGAACG 240
QY 1154 CGAGAGTCTGAAACAAACAAATGAGGCGCAACAGTTCTTACATGTTCTAACTTTGACTT 1213
Db 241 GNNAGTCNAAACAAACAAATGAGGCGCAACAGTTCTTACATGTTCTAACTTTGACTT 300
QY 1214 TGAAACAGTTTTAAACACAGTCTGTTGTCAGCTCCAGTGTGTCTGTCGCGGGGT 1273
Db 301 TGAAACAGTTTTAAACACAGTCTGTTGTCAGCTCCAGTGTGTCTGTCGCGGGGT 359
QY 1274 TGAGTGTGCACTTTTGCCTTTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1333
Db 360 TGAGTGTGCACTTTTGCCTTTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 418
QY 1334 TTGTACTTTTCTATGTTATTAATCTCTGAGAGTCACTAATAAGGAGTATTTTTTTT 1393
Db 419 TTGTAC-TTTTCTATGTTATTAATCTCTGAGAGTCACTAATAAGGAGTATTTTTTTT 477
QY 1394 TGTGAGCTTATCAATCAGACTGATCTAATGTGAATGTAAAGTATCCTTAAA 1444
Db 478 --GCAGCTTATCAATCAGACTGATCTAATGTGAATGTAAAGTATCCTTAAA 526
RESULT 27
AL550164 1053 bp mRNA linear EST 16-FEB-2001
LOCUS AL550164 LTI_NFL006.PL2 Homo sapiens cDNA clone CSODI040YK06 5
DEFINITION AL550164 prime, mRNA sequence.
ACCESSION AL550164
VERSION AL550164.1 GI:12886868
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1053)
REFERENCE
```



**AUTHORS** Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
**TITLE** Full-length cDNA libraries and normalization  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

**FEATURES**  
 source  
 1. 1053  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CS0DI040YK06"  
 /clone\_lib="LTI\_NFL006\_PL2"  
 /tissue\_type="placenta"  
 /notes="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

**BASE COUNT** 198 a 349 c 314 g 191 t 1 others  
**ORIGIN**

Query Match 20.0%; Score 405.8; DB 1; Length 1053;  
 Best Local Similarity 99.3%; Pred. No. 1.3e-92;  
 Matches 410; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAAAGGACAAAGTAAATAAGTACAAATGGTTCGTTCATCAGAGGATACAGTTTCATG 60  
 DB 366 CAAAGGACAAAGTAAATAAGTACAAATGGTTCGTTCATCAGAGGATACAGTTTCATG 425

QY 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGATTAACAGTTACCCCTCAA 120  
 DB 426 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGATTAACAGTTACCCCTCAA 485

QY 121 TGAGCGACCCCTACTCTGTCAGCTATTACCGCGCTGCATTTGGATTTCTTACTCCCTCA 180  
 DB 486 TGAGCGACCCCTACTCTGTCAGCTATTACCGCGCTGCATTTGGATTTCTTACTCCCTCA 545

QY 181 ATGAGGCTCGTGGTCTACTGCGAGGACCCCTCCGATTCATACCTCACCACCTACGGAC 240  
 DB 546 ATGAGGCTCGTGGTCTACTGCGAGGACCCCTCCGATTCATACCTCACCACCTACGGAC 605

QY 241 AGCTCAGTACGGAGACCATATTTATGCAGATGCTGTTTTGGCAGCCTGGGGGCC 300  
 DB 606 AGCTCAGTACGGAGACCATATTTATGCAGATGCTGTTTTGGCAGCCTGGGGGCC 665

QY 301 TGGGGAACAACATCTATCAGCACAGTTCAATTTTTTCCCTGAAACCCCTGCGTTCTCAG 360  
 DB 666 TGGGGAACAACATCTATCAGCACAGTTCAATTTTTTCCCTGAAACCCCTGCGTTCTCAG 725

QY 361 CATGGGGACAAGTGGTCTCAAGGTTCAGCAGACCCAGAGCTCAGCCTCTCCAGCA 417  
 DB 726 CATGGGGACAAGTGGTCTCAAGGTTCAGCAGACCCAGAGCTCAGCCTCTCCAGCA 782

**RESULT 28**  
**AL514504**  
**LOCUS** AL514504 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CL0BB003ZF07 5  
**DEFINITION** Prime, mRNA sequence.  
**ACCESSION** AL514504  
**VERSION** AL514504.1 GI:12777998  
**KEYWORDS** EST.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 977)

**AUTHORS** Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
**TITLE** Full-length cDNA libraries and normalization  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

**FEATURES**  
 source  
 1. 977  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CL0BB003ZF07"  
 /clone\_lib="LTI\_NFL006\_PL2"  
 /tissue\_type="placenta"  
 /notes="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

**BASE COUNT** 191 a 310 c 284 g 181 t 11 others  
**ORIGIN**

Query Match 19.8%; Score 402.2; DB 1; Length 977;  
 Best Local Similarity 96.2%; Pred. No. 1.1e-91;  
 Matches 401; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAAAGGACAAAGTAAATAAGTACAAATGGTTCGTTCATCAGAGGATACAGTTTCATG 60  
 DB 270 CAAAGGACAAAGTAAATAAGTACAAATGGTTCGTTCATCAGAGGATACAGTTTCATG 329

QY 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGATTAACAGTTACCCCTCAA 120  
 DB 330 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGATTAACAGTTACCCCTCAA 389

QY 121 TGAGCGACCCCTACTCTGTCAGCTATTACCGCGCTGCATTTGGATTTCTTACTCCCTCA 180  
 DB 390 TGAGCGACCCCTACTCTGTCAGCTATTACCGCGCTGCATTTGGATTTCTTACTCCCTCA 449

QY 181 ATGAGGCTCGTGGTCTACTGCGAGGACCCCTCCGATTCATACCTCACCACCTACGGAC 240  
 DB 450 ATGAGGCTCGTGGTCTACTGCGAGGACCCCTCCGATTCATACCTCACCACCTACGGAC 509

QY 241 AGCTCAGTACGGAGACCATATTTATGCAGATGCTGTTTTGGCAGCCTGGGGGCC 300  
 DB 510 AGCTCAGTACGGAGACCATATTTATGCAGATGCTGTTTTGGCAGCCTGGGGGCC 569

QY 301 TGGGGAACAACATCTATCAGCACAGTTCAATTTTTTCCCTGAAACCCCTGCGTTCTCAG 360  
 DB 570 TGGGGAACAACATCTATCAGCACAGTTCAATTTTTTCCCTGAAACCCCTGCGTTCTCAG 629

QY 361 CATGGGGACAAGTGGTCTCAAGGTTCAGCAGACCCAGAGCTCAGCCTCTCCAGCA 417  
 DB 630 CATGGGGACAAGTGGTCTCAAGGTTCAGCAGACCCAGAGCTCAGCCTCTCCAGCA 686

**RESULT 29**  
**BB068522**  
**LOCUS** BB068522 RIKEN full-length enriched, 15 days embryo male testis Mus musculus CDNA clone 8030473016.3, similar to AK000398 Homo sapiens CDNA FLJ20391 f18, clone KAI1A4640, mRNA sequence.  
**DEFINITION** BB068522  
**ACCESSION** BB068522  
**VERSION** BB068522.2 GI:15404252  
**KEYWORDS** EST.  
**SOURCE** house mouse.  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.





REFERENCE  
 1 (bases 1 to 441)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 JOURNAL  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)  
 The sequence contained an oligo-dT track that was present in the  
 oligonucleotide that was used to prime the synthesis of first  
 strand cDNA and therefore this may represent a bonafide poly A  
 tail. cDNA library preparation: M.B. Soares Lab Clone distribution:  
 NCI-CGAP clone distribution information can be found through the  
 I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Seq primer: M13 Forward  
 POLYA=Yes.

# FEATURES

Location/Qualifiers  
 1..441  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2713371"  
 /clone\_lib="NCI CGAP Sub3"  
 /lab\_host="DH10B (Life Technologies)"  
 /notes="Vector: p7T3D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The  
 NCI CGAP Sub3 library is a subtracted library derived from  
 the NCI CGAP Sub1 library, which is a subtracted library  
 derived from Bi. BI constitutes a mixture of 21  
 normalized or subtracted NCI CGAP libraries: NCI CGAP\_Co4  
 , NCI CGAP\_Pr22, NCI CGAP\_Pr28, NCI CGAP\_Co10,  
 NCI CGAP\_Co16, NCI CGAP\_Pr28, NCI CGAP\_Co10,  
 NCI CGAP\_Kid5, NCI CGAP\_Kid12,  
 NCI CGAP\_Kid1, NCI CGAP\_Lym2,  
 NCI CGAP\_Br23, NCI CGAP\_Co8, NCI CGAP\_Co11, NCI CGAP\_Le12,  
 NCI CGAP\_Br23, NCI CGAP\_Lu5, NCI CGAP\_Lu24,  
 NCI CGAP\_Lu19, NCI CGAP\_G4, NCI CGAP\_G6,  
 NCI CGAP\_Br25. These 21 libraries were pooled and a  
 single-stranded DNA preparation of the resulting mixture  
 was used as a tracer in a subtractive hybridization with  
 a driver whose composition is detailed below:  
 NCI CGAP\_Kid3 pool 1 LLAM 3334-3337, 3682-3683,  
 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775  
 , 1500552-1502855); NCI CGAP\_Kid5 pool 1 LLAM 3338-3342  
 , 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831,  
 1471368-1472903, 1492104-1493255); NCI CGAP\_Lu5 pool 1  
 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991,  
 1520904-1522439); NCI CGAP\_G4 pool 1 LLAM 3164-3167,  
 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,  
 1469064-1470983, 1475592-1476743); NCI CGAP\_Pr22 pool 1  
 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs  
 985608-986759, 110192-110199, 1217928-1220615);  
 NCI CGAP\_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE  
 CloneIDs 1057416-1061255, 1144584-1145351). Subtraction  
 was performed as previously described [Bonaldo, Lennon &  
 Soares (1996): Normalization and Subtraction: Two  
 Approaches To Facilitate Gene Discovery. Genome Research  
 6, 791-806.  
 TAG\_LIB=NCI CGAP\_Lu5  
 TAG\_TISSUE=Lung\_  
 TAG\_SEQ=CAAC"  
 BASE COUNT 117 a 93 g 131 t  
 ORIGIN

Query Match 19.6%; Score 397.6; DB 2; Length 441;  
 Best Local Similarity 98.8%; Pred. No. 1.3e-90;  
 Matches 411; Conservative 0; Mismatches 1; Gaps 1;  
 QY 979 GAGATTAACACACACCGGTACAACTCCCGGACACCCAGGAGTGCCTTAGAA 1038  
 Db 441 GAGATTAACACACACACCGGTACAACTCCCGGACACCCAGGAGTGCCTTAGAA 382  
 QY 1039 AAAGCCAAAGCAAGTCTGAAATATCAGTTCTCTACAGCACCAACTCCATCTTCGAC 1098  
 Db 381 AAAGCCAAAGCAAGTCTGAAATATCAGTTCTCTACAGCACCAACTCCATCTTCGAC 322

QY 1099 GACTTTGCTCACTACGAGAGCGCCA-GAGAGAGAGAGGTGGTGCAGAAAGACGGCAG 1157  
 Db 321 GACTTTGCTCACTACGAGAGCGCCAGGAGAGAGGTGGTGCAGAAAGACGGCAG 262  
 QY 1158 AGTCGAAACAAACAAATGAGGCGGACAGTTCTTACATGTTCTAAAGTTGACTTTGAA 1217  
 Db 261 CGTCGAAACAAACAAATGAGGCGGACAGTTCTTACATGTTCTAAAGTTGACTTTGAA 202  
 QY 1218 AACAGTTTAAACACAGTGTGCTGGTCCAGTGTGTCGTCCTCCGCGGGGTTGAG 1277  
 Db 201 AACAGTTTAAACACAGTGTGCTGGTCCAGTGTGTCGTCCTCCGCGGGGTTGAG 142  
 QY 1278 TGTTGCACTTTGCTTTCTGTTGCTGTTGTTGTTGTTGCCAGATGATCTGATTTATTTGT 1337  
 Db 141 TGTTGCACTTTGCTTTATTTGCTTTGTTGTTGTTGTTGCCAGATGATCTGATTTATTTGT 82  
 QY 1338 ACTTTTCTATGATTATTAATCTGTAGAAGTCACTAATAAGAGATTTTATTTT 1393  
 Db 81 ACTTTTCTATGATTATTAATCTGTAGAAGTCACTAATAAGAGATTTTATTTT 26

## RESULT 31

AL526609 826 bp mRNA linear EST 13-FEB-2001  
 LOCUS AL526609 LTI\_NFL003\_NBC3 Homo sapiens cDNA clone CS0DC020Y104 5  
 DEFINITION prime, mRNA sequence.  
 ACCESSION AL526609  
 VERSION AL526609.1 GI:12790102  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 826)  
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr).  
 Location/Qualifiers  
 1..826  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CS0DC020Y104"  
 /clone\_lib="LTI\_NFL003\_NBC3"  
 /sex="male"  
 /tissue\_type="neuroblastoma cells"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-stranded cDNA was digested with Not I and  
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
 vector. Library was normalized. Library was constructed  
 by Life Technologies. Contact : Feng Liang Life  
 Technologies, a division of Invitrogen 9800 Medical Center  
 Drive Rockville, Maryland 20850, USA Fax : (1) 301 610  
 8371 Email : [fliang@life.com](mailto:fliang@life.com) URL :  
<http://fulllength.invitrogen.com>

## FEATURES

source  
 1..826  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CS0DC020Y104"  
 /clone\_lib="LTI\_NFL003\_NBC3"  
 /sex="male"  
 /tissue\_type="neuroblastoma cells"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-stranded cDNA was digested with Not I and  
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
 vector. Library was normalized. Library was constructed  
 by Life Technologies. Contact : Feng Liang Life  
 Technologies, a division of Invitrogen 9800 Medical Center  
 Drive Rockville, Maryland 20850, USA Fax : (1) 301 610  
 8371 Email : [fliang@life.com](mailto:fliang@life.com) URL :  
<http://fulllength.invitrogen.com>  
 BASE COUNT 168 a 270 c 239 g 147 t 2 others  
 ORIGIN

Query Match 19.5%; Score 396.4; DB 1; Length 826;  
 Best Local Similarity 98.3%; Pred. No. 3e-90;  
 Matches 411; Conservative 0; Mismatches 6; Indels 1; Gaps 1;  
 QY 1 CAAAGGACAAAGATAAAGTACAAAATGGTTGCTTACATCAGAAGGATACAGTTTCATG 60  
 Db 270 CAAAGGACAAAGATAAAGTACAAAATGGTTGCTTACATCAGAAGGATACAGTTTCATG 329  
 QY 61 CAATGACTTTGAGCCCTACCTTACTCTGGACAGTCAATACAGAGTAAACAGTTACCCCTCAA 120

```

Db 330 ACAATGACTTTGAGCCCTACCTTACTGAGCAGTCAAAATCAGAGTAAACAGTTTACCCCTCAA 389
|||
Qy 121 TGAGCAGCCCTACCTGTCAGCTATTACCCGCGTCCATTGGATTTCCTTACTCCCTCA 180
|||
Db 390 TGAGCAGCCCTACCTGTCAGCTATTACCCGCGTCCATTGGATTTCCTTACTCCCTCA 449
|||
Qy 181 ATGAGGCTCGTGGTCTACTGAGGGGACCTCCGATTCCATACCTCAGCAGCTACGGAC 240
|||
Db 450 ATGAGGCTCGTGGTCTACTGAGGGGACCTCCGATTCCATACCTCAGCAGCTACGGAC 509
|||
Qy 241 AGCTCAGTAACGGAGACCATCATTTTATGACGATGCTGTTTGGGACGCTGGGGCC 300
|||
Db 510 AGCTCAGTAACGGAGACCATCATTTTATGACGATGCTGTTTGGGACGCTGGGGCC 569
|||
Qy 301 TGGGGAACAACAT-CTATCAGCAGCTTCAATTTTTCCTGAAAAACCTGCTGTTCTCA 359
|||
Db 570 TGGGGAACAACATCTATCAGCAGCTTCAATTTTTCCTGAAAAACCTGCTGTTCTCA 629
|||
Qy 360 GCATGGGGACAAGTGGGTCTCAAGTCTCAGCAGACCCAGAGCTCAGCCTTCCCGACA 417
|||
Db 630 GCATGGGGACAAGTGGGTCTCAAGTCTCAGCAGACCCAGAGCTCAGCCTTCCCGACA 687
|||

RESULT 32
AL656188 702 bp mRNA linear EST 13-DEC-2001
LOCUS AL656188 XGC-neurula Silurana tropicalis cDNA clone TNeu035i07 5',
DEFINITION mRNA sequence.
ACCESSION AL656188
VERSION AL656188.1 GI:17668416
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Silurana.
REFERENCE 1 (bases 1 to 702)
Huckle,E., Taylor,R., Ashurst,J.L., Zorn,M.A. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
UNPUBLISHED (2001)
CONTACT: Huckle E
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
TROPICALIS_SEQUENCE_ID: TNeu035i07.sp6
Sequencing primer: Sp6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
FEATURES
Location/Qualifiers
1..702
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu035i07"
/clone_lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from Sug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT 162 a 254 c 185 g 100 t 1 others
ORIGIN
Query Match 19.3%; Score 390.6; DB 1; Length 702;
Best Local Similarity 80.9%; Pred. No. 8.7e-89;
Matches 469; Conservative 0; Mismatches 105; Indels 6; Gaps 1;

Qy 436 CACCCGAGTATCAGAGCCCTCAGCAGCCACCCAGACCGCTGGGTGCCCCACGCAAC 495
|||
Db 129 CCACCCGCCCTCAGCAGCAGCCACAGGCCCTCAGAACCGCTGGGTGGCCCGACGCAAC 188
|||

```

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Qy 496 AGAACAACGGCGCTTTGGGACAGAGCGAGGGGCTGGCAGGATAGCAACTCTCTCTGAAC 555
|||
Db 189 AGGAACCGTCTGTCTACCGCCAGGGCGGAGCGCCGGAGC-----GGAACCTCTGGGCGGG 242
|||
Qy 556 GTCCAGCCTAATTTCTGCCCGCCAGCGTCCGATCCCAACCCCGTCTTTGAAAAAATCTGAAGGT 615
|||
Db 243 GCTCAGTCTTCTCTCGCCCTGGGAACGAGTCCCAACCCCGTCTGGAGAAATCTGAAGGCC 302
|||
Qy 616 GCTCAGCTACAAACCCGAAAGAGTTTGAAGTGAATCTGAAAGCGGGCGTGTGTTCAATC 675
|||
Db 303 GCCCACAGCTACAAACCCCAAGGACTTTGACTGGAACCTGAAAAACGGGCGCGTGTTCATA 362
|||
Qy 676 ATCAAGAGCTACTCTGAGSAGACATCCACCGCTCATTAAGTACTCCATCTGGTGTAGC 735
|||
Db 363 ATAAAGAGCTACTCTCGAGGACGACATCCACCGCTCATTAAGTACTCCATCTGGTGTAGC 422
|||
Qy 736 ACAGAGCAGCGCAACAGCGCTGACAGCGCTTCCGCTGCATGAGCAGCAAGGGGCC 795
|||
Db 423 ACAGAGCAGCGCAACAGCGCTGATAGCGCTTCCGCTGCATGAAACGGCAAGGGGCC 482
|||
Qy 796 GTCTACCTGCTCTTCAAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCCGAGATGAAG 855
|||
Db 483 GTCTACCTGCTCTTCAAGCGTCAACGGCAGCGACACTTCTGCGCGTGGCCGAGATGAAG 542
|||
Qy 856 TCCCGCTGGACTACGACACAGTCCCGGGGTCTGGTCTCAGGACAAAGTGAAGGGGAAG 915
|||
Db 543 TCCCGCTGGACTACGACACAGTCCCGGGGTCTGGTCTCAGGACAAAGTGAAGGGGAAG 602
|||
Qy 916 TTTGATGTCCTGAGTGGATTTTGTAAAGATGTACCAATACCAAGTCCCGCAGCATCAGG 975
|||
Db 603 TTGAGCGTCAAGTGGCTCTTCTGTCNAAGAGCTTCCCAACAGCAGTGGAGGCACATCCGC 662
|||
Qy 976 CTGAGATAACGACAAACAAACCGGTCAAAACTCCCGGG 1015
|||
Db 663 CTGAGACACAGACACACACCGGTCAAAACTCCCGGG 702
|||

RESULT 33
AL524373 820 bp mRNA linear EST 13-FEB-2001
LOCUS AL524373 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC006YG03 5
DEFINITION prime, mRNA sequence.
ACCESSION AL524373
VERSION AL524373.1 GI:12787866
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 820)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
UNPUBLISHED (2001)
CONTACT: Genoscope
Genoscope - Centre National de Sequenage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..820
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC006YG03"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center

```

Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"

BASE COUNT 152 a 242 c 242 g 153 t 31 others  
ORIGIN

Query Match 19.3%; Score 390.6; DB 1; Length 820;  
Best Local Similarity 92.3%; Pred. No. 9.1e-89;  
Matches 395; Conservative 21; Mismatches 11; Indels 0; Gaps 0;

```
QY 1 CAAAGGACAAGATATAAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 60
Db 275 CAAAGGACAAGATATAAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 334
QY 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGAGTACAGTTACCCCTCAA 120
Db 335 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGAGTACAGTTACCCCTCAA 394
QY 121 TGAGCGACCCCTACCTTCCAGCTATTACCGCGCTCCATTTGGATTTCCTTACTCCCTCA 180
Db 395 TGAGCGACCCCTACCTTCCAGCTATTACCGCGCTCCATTTGGATTTCCTTACTCCCTCA 454
QY 181 ATGAGGCTCGGTGTCTATGACGGGACCCCTCGATTCCATCCTCAGACCTACCGGAC 240
Db 455 ATGAGGCTCGGTGTCTATGACGGGACCCCTCGATTCCATCCTCAGACCTACCGGAC 514
QY 241 AGCTCAGTACCGGACCATCATTTTATGACGAGTGTGTTTGGGACGCTGGGGGCC 300
Db 515 AGCTCAGTACCGGACCATCATTTTATGACGAGTGTGTTTGGGACGCTGGGGGCC 574
QY 301 TGGGGAACAACATCTATCAGCACAGGTTCAATTTTTCCTGAAACCCCTGCGTTCTCAG 360
Db 575 TGGGGAACAACATCTATCAGCACAGGTTCAATTTTTCCTGAAACCCCTGCGTTCTCAG 634
QY 361 CATGGGGACAAGTGGGTCTCAAGGTCAGAGCCAGAGCTCAGCTCTCCAGCA 417
Db 635 CATGGGGACAAGTGGGTCTCAAGGTCAGAGCCAGAGCTCAGCTCTCCAGCA 691
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RESULT 34  
AL558224  
LOCUS AL558224 LTI\_NFL008\_Tc2 Homo sapiens cDNA clone CS0DJ001YF07 5  
DEFINITION prime, mRNA sequence.

ACCESSION AL558224  
VERSION AL558224.1 GI:12902542  
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 773)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1. .773

SOURCE

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CS0DJ001YF07"

/clone\_lib="LTI\_NFL008\_Tc2"

/sex="male"

/tissue\_type="T cells from T cell leukemia"

/note="Vector: pCMVSPORT 6; Site 1: NotI; last strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-stranded cDNA was digested with Not I and  
cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
vector. Library was normalized. Library was constructed by  
Life Technologies. Contact : Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive  
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"

BASE COUNT 154 a 260 c 219 g 139 t 1 others  
ORIGIN

Query Match 19.0%; Score 385.4; DB 1; Length 773;  
Best Local Similarity 98.1%; Pred. No. 1.9e-87;  
Matches 411; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

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QY 1 CAAAGGACAAGATATAAAGTACAAATGGTTCGTACATCAGAGGATACAGTTTCATG 60
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QY 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGAGTACAGTTACCCCTCAA 120
Db 337 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGAGTACAGTTACCCCTCAA 396
QY 121 TGAGCGACCCCTACCTTCCAGCTATTACCGCGCTCCATTTGGATTTCCTTACTCCCTCA 180
Db 397 TGAGCGACCCCTACCTTCCAGCTATTACCGCGCTCCATTTGGATTTCCTTACTCCCTCA 456
QY 181 ATGAGGCTCGGTGTCTATGACGGGACCCCTCGATTCCATCCTCAGACCTACCGGAC 239
Db 457 ATGAGGCTCGGTGTCTATGACGGGACCCCTCGATTCCATCCTCAGACCTACCGGAC 516
QY 240 CAGCTCAGTAAACGGACCATCATTTTATGACGAGTGTGTTTGGGACGCTGGGGGCC 299
Db 517 CAGCTCAGTAAACGGACCATCATTTTATGACGAGTGTGTTTGGGACGCTGGGGGCC 576
QY 300 CTGGGGAACAACATCTATCAGCACAGGTTCAATTTTTCCTGAAACCCCTGCGTTCTCA 359
Db 577 CTGGGGAACAACATCTATCAGCACAGGTTCAATTTTTCCTGAAACCCCTGCGTTCTCA 636
QY 360 GCAT-GGGGGACAAGTGGGTCTCAAGGTCAGAGCCAGAGCTCAGCTCTCCAGCA 417
Db 637 GCATGGGGGACAAGTGGGTCTCAAGGTCAGAGCCAGAGCTCAGCTCTCCAGCA 695
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RESULT 35

AL580105/c

LOCUS AL580105 LTI\_NFL008\_Tc2 Homo sapiens cDNA clone CS0DJ001YF07 3

DEFINITION prime, mRNA sequence.

ACCESSION AL580105

VERSION AL580105.1 GI:12945803

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 772)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

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/tissue\_type="T cells from T cell leukemia"

/note="Vector: pCMVSPORT 6; Site 1: NotI; last strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-stranded cDNA was digested with Not I and  
cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,  
a division of Invitrogen 9800 Medical Center Drive  
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :  
<http://fulllength.invitrogen.com>

BASE COUNT 275 a 168 c 148 g 176 t 5 others

## ORIGIN

Query Match 19.0%; Score 384.4; DB 1; Length 772;  
Best Local Similarity 98.3%; Pred. No. 3.4e-87;  
Matches 395; Conservative 4; Mismatches 1; Indels 2; Gaps 1;  
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QY 1687 CAAATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTT 1746  
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QY 1747 TTTTTTTTTTTGAATCTTTCTCCAGATCTGTGCCCCTGGAACGCCACCCGTCC 1806  
Db 652 TTTTTTTTTTT-GAAATCTCTCCCTCCAGATCTGTGCCCCTGGAACGCCACCCGTCC 595  
QY 1807 TCATGTCTCTGTGTCGATTCGGCTGGATGGTGTGGGGCATGATGTGTGAGGAACGTG 1866  
Db 594 TCATGTCTCTGTGTCGATTCGGCTGGATGGTGTGGGGCATGATGTGTGAGGAACGTG 535  
QY 1867 GAAGTGCTTTAGTCTGCTGAGGTGGGCACTTTGTTGTTGGACATCTTTTAA 1926  
Db 534 GAAGTGCTTTAGTCTGCTGAGGTGGGCACTTTGTTGTTGGACATCTTTTAA 475  
QY 1927 ATTTTACACCTTTCTTAAAGATTTCTAATGCGCTCTTAAGTTTATACCAATAATGCTG 1986  
Db 474 ATTTTACACCTTTCTTAAAGATTTCTAATGCGCTCTTAAGTTTATACCAATAATGCTG 415  
QY 1987 AGCTTAAAGTGTAGGATCTGGTAGTACAGACAGATGTGATGGA 2028  
Db 414 AGCTTAAAGTGTAGGATCTGGTAGTACAGACAGATGTGATGGA 373

RESULT 36  
AW766504/c  
LOCUS  
DEFINITION  
da63d11.xl Harland stage 19-23 Xenopus laevis cDNA clone  
IMAGE:3199605 3' similar to TR:064526 064526 YUP8H12R.13 PROTEIN.  
; mRNA sequence.

ACCESSION  
VERSION  
AW766504.1 GI:7698494

KEYWORDS  
EST.

SOURCE  
African clawed frog.

ORGANISM  
Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 659)

Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pabe, D.,

Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person

, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, J., McCann, R.,

Waterston, R. and Wilson, R.

WashU Xenopus EST project, 1999

Unpublished (1999)

Other ESTs: da63d11.v1

Contact: Sandy Clifton, Ph.D.

WashU Xenopus EST project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)

Library constructed by R. Harland, PhD (University of California,

Berkeley)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available  
through the I.M.A.G.E. Consortium/LNLN at:  
[image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)  
Seq primer: -40UP from Gibco  
High quality sequence stop: 503.

## FEATURES

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; cDNA made by oligo-dT priming. Library constructed by  
Dr. Francesca Mariani in the laboratory of R. Harland,  
Ph.D. (University of California, Berkeley). References:  
XBP-2 is a transcriptional repressor that converts  
ectoderm into neural tissue. Mariani, F.V. Harland, R.M.,  
Development. 1998 Dec;125(24):5019-31. PMID: 9811586; UI:  
99030283; Use of large-scale expression cloning screens in  
the xenopus laevis tadpole to identify gene function.  
Grammer TC, Liu KJ, Mariani FV, Harland RM, Dev Biol.  
2000 Dec 15;228(2):197-210. PMID: 11112324; UI: 20564075;  
Note: This is a Xenopus Gene Collection (XGC) library."

BASE COUNT 148 a

161 c

153 g

196 t

1 others

ORIGIN

Query Match 17.9%; Score 363; DB 2; Length 659;

Best Local Similarity 82.5%; Pred. No. 9e-82;

Matches 439; Conservative 0; Mismatches 91; Indels 2; Gaps 2;

QY 625 TACAACCCGAAAGAGTTTGGTGGAAATCTGAAAACGGCGGTGTTCATCATCAAGAGC 684

Db 659 TATAACCTTAGGATTTTGGTGGAACTTGAATAATGACGTGTCTTATATTAAGAGT 600

QY 685 TACTCTGAGGACGACATCCACGGCTCCATTAAGTACTCCATCTGCTGTAGCAGAGCAC 744

Db 599 TATT-TGAGGATGATATCCCGNGTTCCATCATATTCATTTGGTCAGCAGCAGCAT 541

QY 745 GGCAACAAGCGCTCGACAGCGCTTCGCTCATGAGCAGCAAGGGCCCGCTTACCTG 804

Db 540 GGGATAAAGCGTTGGATAACGCTTTCCGCTCCATGAATGGCAAGGGCCCGCTTACCTT 481

QY 805 CTCTTCAGCGCTCAATGGGAGTGGGCATTTTGTGGGGTGGCGAGATGAAGTCCCGCTG 864

Db 480 CTGTTGCGGTACAGCGAGTGGACACTTTTGGCGGTAGCCGAGATGAAGTCCCGCTG 421

QY 865 GACTACGGCACCAGTCCCGGGGTCTGGTCTCAGGACAAAGTGAAGGGGAAGTTTGAATGC 924

Db 420 GACTATGGCACCAGTCCCGGTCTGTGTGCACAGGACAAATGCAAGGGCAAGTTTGCAGTC 361

QY 925 CAGTGGATTTTGTAAAGATGTACCCAAATACAGCTCCGCGACATCAGGCTGGAGAT 984

Db 360 AAGTGGCTCTTTGTCAAGGACCTTCCCAACACAGCTGAGGACATCCGCTGGAGAT 301

QY 985 AACGACACAACCCGTCAAACTCCCGGGACACCCAGAGGTGCCCTTAGAAAAGCC 1044

Db 300 AACGACACAACCCGGTCAAACTCCCGAGACACGAGAGGTGCCCTTAGAAAAGCA 241

QY 1045 AAGCAAGTGTGAAAATATCAGTTCTTACAGACACAACTCCATCTTCGACGACTTT 1104

Db 240 AACTGTGTCTTAATCATTCCTCCACTTACAGACACAGACCTCCATCTTTGATGACTTT 181

QY 1105 GCTCTACTAGAGAGCGGCA-CAGGAGGAGGAGGTGGTGGCGCAAGAACGGC 1155

Db 180 TCTCATTACGAGAGCGGAGGAGGAGGAGGTGTGCGCAAGGTAAACGC 129

RESULT 37

BS542677

LOCUS

BE542677

790 bp

mRNA

linear

EST 09-AUG-2000

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DEFINITION 601067173F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453235 5',
mRNA sequence.
ACCESSION BE542677
VERSION BE542677.1 GI:9771322
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgs.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LL8436 row: b column: 20
High quality sequence stop: 632.
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Location/Qualifiers
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 kb. Library prepared by Life
Technologies."
BASE COUNT 187 a 222 c 226 g 155 t
ORIGIN
Query Match 17.8%; Score 361.8; DB 2; Length 790;
Best Local Similarity 97.7%; Pred. No. 1.9e-81;
Matches 388; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
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DB 1 ACAAATGGTTCGTTACATCAGAGGATACAGATTCATGACAAATGACATTTGAGCCCTACCT 60
QY 83 TACTGGACAGTCAAAATCAGAGTAACAGTTACCCCTCAATGAGCGACCCCTACCTGTCCAG 142
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QY 262 ATTTTATG-CACGATGCTGTTTTTGGGAGCGCTGGGGCCCTGGGGAAACACATCATTCAG 320
DB 241 ATTTTATGTCACGATGCTGTTTTTGGGAGCGCTGGGGCCCTGGGGAAACACATCATTCAG 300
QY 321 CACAGGTTCAATTTTTTCCCTGAAACCCCTGCGTTCTCAGCATGGGGGACAAAGTGGTCT 380
DB 301 CACAGGTTCAATTTTTTCCCTGAAACCCCTGCGTTCTCAGCATGGGGGACAAAGTGGTCT 360
QY 381 CAGGTCAGCAGACCCAGAGCTCAGCCTCTCCACGA 417
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BB610489  
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musculus cDNA clone 2210410K23 5', mRNA sequence.  
BB610489  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

1010 bp mRNA linear EST 26-OCT-2001  
BB610489 RIKEN full-length enriched, adult male stomach Mus  
musculus cDNA clone 2210410K23 5', mRNA sequence.  
BB610489.1 GI:16452007  
EST.  
house mouse.  
Mus musculus  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT

Unpublished (2001)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsr.riken.go.jp  
URL: http://genome.gsc.riken.go.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh  
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura  
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara  
Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-299 (2001)  
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa  
K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and  
Hayashizaki, Y.  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.  
e mouse tissues.  
Location/Qualifiers  
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Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer 15'

FEATURES  
source

BB610489  
LOCUS  
DEFINITION  
musculus cDNA clone 2210410K23 5', mRNA sequence.  
BB610489  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

1010 bp mRNA linear EST 26-OCT-2001  
BB610489 RIKEN full-length enriched, adult male stomach Mus  
musculus cDNA clone 2210410K23 5', mRNA sequence.  
BB610489.1 GI:16452007  
EST.  
house mouse.  
Mus musculus  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT

Unpublished (2001)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsr.riken.go.jp  
URL: http://genome.gsc.riken.go.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh  
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura  
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
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RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara  
Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
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Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa  
K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and  
Hayashizaki, Y.  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.  
e mouse tissues.  
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/dev\_stage="adult"  
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Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer 15'

FEATURES  
source

BB610489  
LOCUS  
DEFINITION  
musculus cDNA clone 2210410K23 5', mRNA sequence.  
BB610489  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

1010 bp mRNA linear EST 26-OCT-2001  
BB610489 RIKEN full-length enriched, adult male stomach Mus  
musculus cDNA clone 2210410K23 5', mRNA sequence.  
BB610489.1 GI:16452007  
EST.  
house mouse.  
Mus musculus  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT

Unpublished (2001)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsr.riken.go.jp  
URL: http://genome.gsc.riken.go.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh  
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura  
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara  
Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-299 (2001)  
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa  
K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and  
Hayashizaki, Y.  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.  
e mouse tissues.  
Location/Qualifiers  
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/organism="Mus musculus"  
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/lab\_host="SOLR"  
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prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer 15'

FEATURES  
source

BB610489  
LOCUS  
DEFINITION  
musculus cDNA clone 2210410K23 5', mRNA sequence.  
BB610489  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

1010 bp mRNA linear EST 26-OCT-2001  
BB610489 RIKEN full-length enriched, adult male stomach Mus  
musculus cDNA clone 2210410K23 5', mRNA sequence.  
BB610489.1 GI:16452007  
EST.  
house mouse.  
Mus musculus  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT

Unpublished (2001)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsr.riken.go.jp  
URL: http://genome.gsc.riken.go.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh  
M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura  
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
Hayashizaki, Y.  
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sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara  
Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-299 (2001)  
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa  
K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and  
Hayashizaki, Y.  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.  
e mouse tissues.  
Location/Qualifiers  
1..1010  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="2210410K23"  
/clone\_lib="RIKEN full-length enriched, adult male  
stomach"  
/sex="male"  
/tissue\_type="stomach"  
/dev\_stage="adult"  
/lab\_host="SOLR"  
/notes="Site 1: XhoI; Site 2: SstI; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer 15'

FEATURES  
source

GAGAGAGAGCGCGCGCACTCGAGTTTTTTTTTTTTTTTTTTTTTTVN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGAGTTATTAATTAATATCCCCCCCCCC 3']. cDNA was cycled with XhoI and SstI."

BASE COUNT 218 a 292 c 276 g 223 t 1 others  
ORIGIN

Query Match 17.0%; Score 345; DB 2; Length 1010;  
Best Local Similarity 89.2%; Pred. No. 3.9e-77;  
Matches 372; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAAGGCAAGATAAAGTACAAATGGTTCGTATACAGAGGATACAGTTTCATG 60  
Db 237 CAAAGGCAAGATAAAGTACAAATGGTTCGTATACAGAGGATACAGTTTCATG 296

Qy 61 ACATGACTTTGAGCCCTACCTTACTGACAGTCAAAATCAGAGTACAGTTACCCCTCAA 120  
Db 297 ACAATGACTTTGAGCCCTACCTTCTGGACAGTCCAAATCCGAGTACAGTTACCCCTCGA 356

Qy 121 TGAGCGACCCCTACCTGTCAGCTATTACCGCGCTGCAATTCGATTCCTTACTCCCTCA 180  
Db 357 TGAGTGATCTTTACCTGTCAGTACTATCCACCATCCATTCGATTCCTTACTCCCTCA 416

Qy 181 ATGAGGCTCCGTGTTACTGAGGGGACCTCCGATTCATCCATCCTCACCACTACGGAC 240  
Db 417 GCGAGGACCATGGTCCACTGACGGGACCTCCCATCCGTTATCTCACTACTATGGAC 476

Qy 241 AGCTCAGTAAACGAGACCATCATTTTATGACAGTCTGTTTTGGGAGCTGGGGGCC 300  
Db 477 AACTTAGTAATGAGACCATCACTTTCATGATGCTGTTTTGGGAGCTGGGGGTC 536

Qy 301 TGGGGAACACATCTATGACACAGTTCATTTTTCCTGAAACCTGCTTCTCAG 360  
Db 537 TGGGGAACACATTTTACCAGACAGGTTTAAATTTTTCCTGAAACCTGCAATTCAG 596

Qy 361 CATGGGGGCAAGTGGTCTCAAGGTTCAGAGACCCAGAGCTCAGGCTCTCCAGCA 417  
Db 597 CATGGGGGCAAGTGGTCTCAGGGGACAGACTCAGAGCTCAGGCTATGGAGCA 653

RESULT 39  
AL515909  
LOCUS  
DEFINITION AL515909 LTI\_NFL011\_NBC1 Homo sapiens cDNA clone CS0DA001YB18 5 prime, mRNA sequence.

ACCESSION AL515909  
VERSION AL515909.1 GI:12779402  
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES location/Qualifiers

1..917

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CS0DA001YB18"

/clone\_lib="LTI\_NFL011\_NBC1"

/sex="male"

/tissue\_type="neuroblastoma cells"

/lab\_host="DH108"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 174 a 274 c 228 g 206 t 35 others  
ORIGIN

Query Match 16.7%; Score 338; DB 1; Length 917;  
Best Local Similarity 88.8%; Pred. No. 2.3e-75;  
Matches 366; Conservative 17; Mismatches 27; Indels 2; Gaps 2;

Qy 1 CAAAGGCAAGATAAAGTACAAATGGTTCGTATACAGAGGATACAGTTTCATG 60  
Db 278 CAAAGGCAAGATAAATGTTTACAAATGGTTCGTATACATCATAGGWTATATTTCAT 337

Qy 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAAAATCAGAGTAAACAGTTACCCCTCAA 120  
Db 338 AYATATATTTTACCTTACTGGACATTTAAATYAGATTTTACATTACCCCTYAA 397

Qy 121 TGAGCGACCCCTACCTGTCAGCTATTACCGCGCTGCCATTGGATTTCTTACTCCCTCA 180  
Db 398 TTAGCTACCCCTACCTTTCAGCTATTATYCGYTTTATTGGATTCTTACTCCCTCA 457

Qy 181 ATGAGGCTCCGTG-TCTACTGCGAGGACCTCCGATTCATCCATCCTCACCACTACCGA 239  
Db 458 ATGAGGCTCCGTGTCATTTCTGGTACCTCCGATTCATCCTCACCACTACCGA 517

Qy 240 CAGCTCAGTAAACGAGACCATCATTTTATGACAGTATGTTTTGGGAGCTGGGGGC 299  
Db 518 CAGCTCAGTAAACGAGACCATCATTTTATGACAGTATGTTTTGGGAGCTGGGGGC 577

Qy 300 CTGGGGAACAACATCTATCAGCAGGTTCAATTTTTTCCCTGAAAAACCTCGGTTCTCA 359  
Db 578 CTGGGGAACAACATCTATCAGCAGGTTCAATTTTTTCCCTGAAAAACCTCGGTTCTCA 637

Qy 360 GCAT-GGGGAGCAAGTGGTCTCAGGTCAGCAGACCCAGAGCTCAGGCTCT 410  
Db 638 GCATGGGGGAGCAAGTGGTCTCAGGTCAGCAGACCCAGAGCTCCGGGTAT 689

RESULT 40

AA460050

LOCUS

DEFINITION

AA460050 355 bp mRNA linear EST 09-JUN-1997  
zx66c02.r1 Soares total fetus NB2HF8 9w Homo sapiens cDNA clone  
IMAGE:796418 5' similar to TR:G849195 G849195 CHROMOSOME IV COSMID  
9481.; mRNA sequence.

ACCESSION

AA460050

VERSION

AA460050.1 GI:2184934

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 355)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,

Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,

T., Waterston, R. and Wilson, R.

WashU-Merck EST Project 1997

Unpublished (1997)

CONTACT: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LLNL; contact the



Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Thetaling, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.









QY 1492 TTGATATTCTGTGAGACTTCATATTTCTCATCCCTTTATTCCTTTTGTAGCAACATAGA 1551  
DB 120 TTGATATTCTGTGAGACTTCATATTTCTCATCCCTTTATTCCTTTTGTAGCAACATAGA 179  
QY 1552 AACCATGAGTCATTTTGTCAATTTAGAGTATTTCTGATAAAATCTCTTGAAAAATCTGAAAT 1611  
DB 180 AACCATGAGTCATTTTGTCAATTTAGAGTATTTCTGATAAAATCTCTTGAAAAATCTGAAAT 239  
QY 1612 CAAAGGTTAATGATTTTGTTCATCTGATTTTGTCAATTTTATATCTGTTATCGGFTCT 1671  
DB 240 CAAAGGTTAATGATTTTGTTCATCTGATTTTGTCAATTTTATATCTGTTATCGGFTCT 299  
QY 1672 AAAGTGTCAATTTTACCATTTGATTTTCTGCTAGACAG 1710  
DB 300 AAAGTGTCAATTTTACCATTTGATTTTCTGCTAGACAG 338

RESULT 47  
LOCUS  
AW465438  
DEFINITION  
BP230019A20B7 Soares normalized bovine placenta Bos taurus cDNA  
clone BP230019A20B7 5', mRNA sequence.  
ACCESSION  
AW465438  
VERSION  
AW465438.1 GI:7035606  
KEYWORDS  
EST.  
SOURCE  
cow.  
ORGANISM  
Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
1 (bases 1 to 521)  
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardini,J., Liu,L. and Larson  
J.H.  
Bovine ESTs  
Unpublished (2000)  
Contact: Lewin, H. A.  
W. M. Keck Center for Comparative and Functional Genomics  
University of Illinois at Urbana-Champaign  
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL  
61801, USA  
Tel: 217 333 5998  
Fax: 217 244 5617  
Email: h-lewin@uiuc.edu

Funding for cattle EST sequencing was provided by the USDA National  
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534  
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED  
from Washington University Genome Center. Vector Trimmi g:  
Crossa match from Washington University Genome Center PHRAP suite.  
Sequences submitted are vector free and at least 200 bp in length.  
PCR Primers  
FORWARD: TAATACGACTCACTATAGG  
BACKWARD: ATTAACCTCTCACTAAG  
Insert Length: 521 Row Error: 0.00  
Plate: BP230019A20 Row: B Column: 7  
Seq primer: AGCGGATACATTTACACAGGA  
High quality sequence stop: 521.  
Location/Qualifiers  
1. .521  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone="BP230019A20B7"  
/sex="female"  
/lab\_host="DH10B"  
/notes="Organ: placenta; Vector: pT7T3Pac; Site 1: EcoRI;  
Site 2: NotI; The cDNA library was constructed by the  
Soares laboratory and it was constructed and normalized  
as described by Bonaldo, M.F., Lennon, G. and Soares,  
M.B. (1996), Genome Research 6(9): 791-806."

BASE COUNT  
ORIGIN  
150 a 119 c 124 g 128 t

Query Match 15.7%; Score 319.4; DB 2; Length 521;  
Best Local Similarity 75.8%; Pred. No. 1.1e-70;  
Matches 395; Conservative 0; Mismatches 126; Indels 0; Gaps 0;  
QY 594 CGTCTTTGAAAAAAGCTGAAGGCTGCTCACAGCTACAAACCGAAAGAGTTTGTAGTGGAACTCT 653  
DB 1 CGTCTTTGAGAGAGCTTCGGTCCATTAACTATTAACCCNAGGATTTTGTAGTGGAACTCT 60  
QY 654 GAAAGCGGCGGTGTGTTCATCATCAAGAGCTACTCTTGAGGACGACATCCACCGCTCCAT 713  
DB 61 GAAACATGCGCGGGTTTTCATCATTAAGAGCTACTCTCGAGGACGATATCCACCGTTCCAT 120  
QY 714 TAAGTACTTCCATCTGTTGAGGACGAGCAGGCAACAGCGCTGAGCAGCGCTTCCG 773  
DB 121 TAAGTATAATATCTGTTGAGGACGAGCAGGCAATGTTAAAGAGAGCTGGATGCTGTTATCG 180  
QY 774 CTGCATGAGCAGCAAGGGGCGGCTCTACCTGCTCTTCCAGGCTCAATGGGAGTGGGCACTTT 833  
DB 181 CTCATGACGAGGAGGAGGCGGCTTACTTTTCTGTTTCAACCGGAGTGACACTT 240  
QY 834 TTGTGGGTGGCGGAGATGAAGTCCCGGTGGACTACGGCAGCAGTCCCGGGTCTTGGTC 893  
DB 241 CTGTGGGTGTCGAGAAATGAAATCTGCTGTGGACTACACACATGTSCAGGTGTGGTC 300  
QY 894 TCAGGACAACTGGAAGGGAAGTTTGTATGTCAGTGGATTTTGTAAAGATGTACCCAA 953  
DB 301 CCAGGACAAATGGAAGGCGGCTTTTGTATGTGAGTGGATTTTGTGAAGCAGCTTCCAA 360  
QY 954 TAACCACTCCGCGACATCAGCTGGAGATACGACAAACACCGGTCTCAAACTCCG 1013  
DB 361 TAGCCAACTCGGACATCTCCCTAGAGAACAGGAGATTAACCGAGTACCAACTCCAG 420  
QY 1014 GGACACCCAGGAGTGGCTTTAGAAAAAGCAAGCAAGTGTGAAAAATTTATCAGTTCTTA 1073  
DB 421 GGACACTCAGGAGTGGCTCTCGAAAAAGCTAAGCAGGTGTTGAAAAATCATAGCCAGTA 480  
QY 1074 CAGGACACAACTCCATCTTTCGACGACTTTGCTCACTACG 1114  
DB 481 CAAGCACCACCTTCCATTTTGTATGATGACTTCTCACACTATG 521

RESULT 48  
LOCUS  
AV711963  
DEFINITION  
AV711963 DCA Homo sapiens cDNA clone DCAAABC07 5', mRNA sequence.  
ACCESSION  
AV711963  
VERSION  
AV711963.1 GI:10731269  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 383)  
Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,  
Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,  
Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu  
G., Cheng,Z. and Han,Z.  
Homo sapiens cDNA DCA clones  
Unpublished (2000)  
Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919 (ex.45)  
Fax: 86-21-50801922  
Email: hanzg@hgc.sh.cn  
This clone is available at CHGC in Shanghai.

FEATURES  
source  
1. .383  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="DCAAABC07"  
/clone\_lib="DCA"

/cell\_type="dendritic cells"  
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/lab\_host="BM25.8"  
/note="Vector: pTriplEx2; Site\_1: sfIIA; Site\_2: sfIIB"  
BASE COUNT 91 a 53 c 77 g 162 t  
ORIGIN

Query Match 15.6%; Score 316.4; DB 2; Length 383;  
Best Local Similarity 87.2%; Pred. No. 5.7e-70;  
Matches 382; Conservative 0; Mismatches 1; Indels 55; Gaps 1;  
QY 1570 CATTAGAGTATCTCATAAATCTCTGAAATATCTGAATCAAAAGGTTAATGATTTT 1629  
Db 1 CATTAGAGTATCTGATAAATCTCTGAAATATCTGAATCAAAAGGTTAATGATTTT 60  
QY 1630 TTGTCATTTCTGATTTGTCATTTTATTATCTGTTATCGGTCTAAAGTGTCTAAATACCCA 1689  
Db 61 TTGTCATTTCTGATTTGTCATTTTATTATCTGTTATCGGTCTAAAGTGTCTAAATACCCA 120  
QY 1690 TTGATTTTCTGCTAGACAGATAACTTTTAAATTTTCAAAATTTGGCAGACATTTT 1749  
Db 121 TTGATTTTCTGCTAGACAGATAACTTTTAAATTTTCAAAATTTGGCAGACATTTT 180  
QY 1750 TTTTCTTGAATCTTCTCTCCAGATCTGTTGCCACTGAACAGCCCGCTCCCTCA 1809  
Db 181 TTTTCTTGAATCTTCTCTCCAGATCTGTTGCCACTGAACAGCCCGCTCCCTCA 186  
QY 1810 CTGCTCTGTTCCGATTTGGCTGGATGTTGGGCGATGATGTTGGAGGAATCGGAA 1869  
Db 187 -TGCTCTGTTCCGATTTGGCTGGATGTTGGGCGATGATGTTGGAGGAATCGGAA 245  
QY 1870 GGTGCTTTAGTCTGTTGAGGTCGGGCAATCTTTGTTGTTGGCAGATCTTTTAAAT 1929  
Db 246 AGTGCTTTAGTCTGTTGAGGTCGGGCAATCTTTGTTGTTGGCAGATCTTTTAAAT 305  
QY 1930 TTACACCTTTCTTGAATCTTAATCGCTTAAGTTTATACCAATATGCTGAGC 1989  
Db 306 TTACACCTTTCTTGAATCTTAATCGCTTAAGTTTATACCAATATGCTGAGC 365  
QY 1990 TTTAAGTGTAGGATCTGG 2007  
Db 366 TTTAAGTGTAGGATCTGG 383

RESULT 49  
LOCUS BE089793 340 bp mRNA linear EST 12-JUN-2000  
DEFINITION RC5-BT0707-150300-021-E10 BT0707 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BE089793  
VERSION BE089793.1 GI:8480229  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 340)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=&t2=RC5-BT0707-150  
300-021-E10&t3=2000-03-15&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 339.  
Location/Qualifiers  
1. 340  
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/db\_xref="taxon:9606"  
/clone\_lib="BT0707"  
/dev\_stage="Adult"  
/note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."  
BASE COUNT 100 a 55 c 51 g 134 t  
ORIGIN

Query Match 15.6%; Score 315.8; DB 2; Length 340;  
Best Local Similarity 99.4%; Pred. No. 7.8e-70;  
Matches 317; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1418 CTAATGTGAATGTAAAGTATCTTAAACAAAGCATCTATTTTGGCAGAAATTTGTTTC 1477  
Db 4 CAATGTGAATGTAAAGTATCTTAAACAAAGCATCTATTTTGGCAGAAATTTGTTTC 63  
QY 1478 TTAATTTCACTGATTTGATTTCTGTGAGACTTCATTTTCACTCCCTTTATGCTTTT 1537  
Db 64 TTAATTTCACTGATTTGATTTCTGTGAGACTTCATTTTCACTCCCTTTATGCTTTT 123  
QY 1538 TAGCAACATAGAACCATGATGATTTTCTCATTTAGAGTATCTGTATTAATCTCTT 1597  
Db 124 TAGCAACATAGAACCATGATGATTTTCTCATTTAGAGTATCTGTATTAATCTCTT 183  
QY 1598 GAAATACTGAAATCAAAAGGTTAATGATTTTGTGTTCTCATTTCTGATTTTATTA 1657  
Db 184 GAAATACTGAAATCAAAAGGTTAATGATTTTGTGTTCTCATTTCTGATTTTATTA 243  
QY 1658 TCTGTTATCGGTCTAAAGTCTAATTTACCCATTTGATTTTCTGTAGACATTAATT 1717  
Db 244 TCTGTTATCGGTCTAAAGTCTAATTTACCCATTTGATTTTCTGTAGACATTAATT 303  
QY 1718 TTAATTTTCAAAATTTGGC 1736  
Db 304 TTAATTTTCAAAATTTGGC 322

RESULT 50  
LOCUS AV757830 780 bp mRNA linear EST 19-OCT-2000  
DEFINITION AV757830 BM Homo sapiens cDNA clone BMFAW05 5', mRNA sequence.  
ACCESSION AV757830  
VERSION AV757830.1 GI:10915678  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 780)  
AUTHORS Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H.,  
Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng  
L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G.,  
Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z.  
TITLE Homo sapiens cDNA BM clones  
JOURNAL Unpublished (2000)  
COMMENT Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.

FEATURES  
source  
1. .780  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="BMFAWB05"  
/clone\_lib="BM"  
/tissue\_type="Bone marrow"  
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/lab\_hosts="BM25.8"  
/notes="Vector: pTriplEx2; Site 1: sfIIA; Site 2: sfIIB"  
BASE COUNT 234 a 147 c 170 g 226 t 3 others  
ORIGIN

Query Match 15.2%; Score 307.8; DB 2; Length 780;  
Best Local Similarity 75.1%; Pred. No. 1.1e-67;  
Matches 384; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 629 ACCGGAAGAGTTTGGTGGAACTCTGAAAGCGGCGTGTTCATCATCAAGAGCTACT 688  
DB 72 ATCCCAAGACTTTGATGGATCTGAAGATGAGCGTGTGTATATTTAAAGCTACT 131  
QY 689 CTGAGGACGATCCACCGTCTCCATTAAAGTACTCCATCTGTGTAGCAGACGCGCA 748  
DB 132 CTGAGGATGACATACATCGTTTCCATTAAATACTCTATCTGTGTAGTACTGAGCATGTA 191  
QY 749 ACAAGCCCTGGACAGCGCTTCCGCTGTCATGACGACGAGGGGCCGCTACTGCTCT 808  
DB 192 ATAAGCGTTTGGATGCGACTTACCGTTCCCTGAAATGGGAAAGGCCACTCTATTTACTCT 251  
QY 809 TCAGCGTCAATGGAGTGGGCAATTTTGTGGGCGCGAGATGAAGTCCCGCTGACT 868  
DB 252 TCAGTGTGAATGGCAGTGGACATTTTGTGGAGTGGCTGAAATGAAGTCTGTGTGACT 311  
QY 869 ACGSCACAGTCCCGGGTCTGTGTCTCAGGACAAAGTGAAGGGGAAGTTTGTATCCAGT 928  
DB 312 ATAATGCGTATGCTGGTGTCTGGTCTCAGGATAAGTGGAGGGCAAAATTTGAAGTTAAAT 371  
QY 929 GGATTTTGTAGGATGTACCCCAATACCGACTCCGGCACATCAGGCTGGAGAAATACG 988  
DB 372 GGATCTTTGTCAAGATGTTTCCCAATACCAATTAACGGCATATTTCGCTTAGAAAATAATG 431  
QY 989 ACAACAAACCGTCCACAACTCCCGGACACCCAGGAGGTGCCCTTAGAAAAAGCCAAAGC 1048  
DB 432 ACAACAAACCGTTCACCAATTCAGGGACACTCAAGAGGTACCCCTAGAAAAAGCTAAGC 491  
QY 1049 AAGTGTGAAAAATPATCAGTTTCTTACAAGCACACAACCTCCATCTTCGACGACTTTGCTC 1108  
DB 492 AAGTGTCTAAAATAATTGCTACTTTCAAGCATACCACTCAATCTTTGATGACTTTGAC 551  
QY 1109 ACTACGAGAGCGCCAGAGGAGGAGGAGGTG 1139  
DB 552 ATTATGCGCTCAAGAGAGGAGGAGGAGCCATG 582

RESULT 51  
BE242919 326 bp mRNA linear EST 03-OCT-2001  
LOCUS TCAAP1E2446 Pediatric acute myelogenous leukemia cell (FAB M1)  
DEFINITION Baylor-HGSC project=TCAA Homo sapiens cdna clone TCAAP2446, mRNA sequence.  
ACCESSION BE242919  
VERSION BE242919.1 GI:9094652  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 326)

AUTHORS Wei, Y., Tsang, Y. T. M., Mei, G., Ku, J. M., Ali-Osman Jr., F. R., Muzny, D., Bouck, J., Gibbs, R. A. and Margolin, J. F.  
TITLE Pediatric Leukemia cDNA Sequencing Project  
JOURNAL Unpublished (2000)  
COMMENT Contact: Dr. Judith F. Margolin  
Texas Children's Cancer Center and Human Genome Sequencing Center  
at Baylor College of Medicine  
1102 Bates, MC3-3320 Houston, TX 77030, USA  
Tel: 832-824-4536  
Fax: 832-825-4038  
Email: clones@ccc.org  
Citation: Carninci, P. and Hayashizaki, Y. High efficiency  
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Seq primer: M13 primer.  
Location/Qualifiers  
1. .326  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="TCAAP2446"  
/clone\_lib="Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA"  
/sex="male"  
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/cell\_type="myeloid cell"  
/dev\_stage="pediatric 6 years"  
/lab\_host="DH10B"  
/notes="Vector: lambda pSB; Site 1: BamHI; Site 2: EcoRI;  
First strand cDNA was primed with an anchored  
XhoI-oligo(dT) primer [5'GGAGACTCGAGCGCGCGCAGGAG(T)VN  
3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand  
was primed with a BamHI-8C primer  
[5'AGAGACTCGATCCCGCGCAATAATAAT(C) 3'].  
Double-stranded cDNA was then digested with BamHI and XhoI  
and directionally cloned into the BamHI and SalI sites of  
lambda pSB vector. Library went through one round of  
normalization. Library was constructed by Wei Yu at RIKEN  
of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T,  
Itoh M, Nagaoaka S, Sasaki, Okazaki Y, Muramatsu M,  
Schneider C, Hayashizaki Y, High efficiency selection of  
full-length cDNA by improved biotinylated cap trapper.,  
DNA Res 4: 1, 61-6, Feb 28, 1997)."  
BASE COUNT 75 a 97 c 77 g 77 t  
ORIGIN

Query Match 15.1%; Score 307; DB 2; Length 326;  
Best Local Similarity 96.9%; Pred. No. 1.3e-67;  
Matches 313; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 95 AAATCAGAGTAAAGTTTACCCCTCAATGAGCGACCCCTACCTGCCAGCTATTACCGCC 154  
DB 2 AAATCAGAGTAAAGTTTACCCCTCAATGAGCGACCCCTACCTGCCAGCTATTACCGCC 61  
QY 155 GTCATTGGATTTCCCTACTCTCCCTCAATGAGGCTCGTGTCTACTGCGGGGACCCCTCC 214  
DB 62 GTCATTGGATTTCCCTACTCTCTATTGAGGCTCGTGTCTACTGCGGGGACCCCTCC 121  
QY 215 GATTTCATACCTCACCACCTTACGAGACGCTCAGTAACGAGACCATCATTTTATGCACGA 274  
DB 122 GATTTCATACCTCACCACCTTACGAGACGCTCAGTAACGAGACCATCATTTTATGCACGA 181  
QY 275 TGTGTTTTTGGGACGCTGGGGCCCTGGGGAAACAATCATCTATCAGCACAGGTTCAATTT 334  
DB 182 TGTGTTTTTGGGACGCTGGGGCCCTGGGGAAACAATCATCTATCAGCACAGGTTCAATTT 241  
QY 335 TTTTCCCTGAAACCCCTGCGTTCTCAGCATGGGGGCAAGTGGCTCTCAGGTTCAGGAC 394  
DB 242 TTTTCCCTGAAACCCCTGCGTTCTCAGCATGGGGGCAAGTGGGTCTCTCAAGGTTCAGGAC 301  
QY 395 CCAGAGCTCAGCCTCTCCACGCA 417  
DB 302 CCAGAGCTCCGGTATGGGAGCA 324

Qy 539 GCAACTCTCTGGAAACGTCCAGCCTAATTCTGCCCCAGCGTCGAATCCACACCCCGTCC 598



```

Db      4  GGAACCCCTTTGGGAGGAGTCCAGCCTCATGCTGCCCTGGAAACGAATCTCACCTCTGC 63
Qy      599  TTGAAAACACTGAAGCGCTCTCACAGCTACAAACCCGAAAGAGTTTGAAGTGAATCTGAAAA 658
Db      64  TAGAGAACTGAAGCGCTCCACAGCTACAAACCCAGGAGCTTTGACTGGAACTGAAA 123
Qy      659  GCGGGCGTGTTCATCATCAAGAGCTACTCTGAGGAGGAGCATCCACCGCTCCATTAAGT 718
Db      124  ATGACGCTGTGTTTATATAAAGAGCTATTCTGAGGATGATATCCACCGTTCCATCAAT 183
Qy      719  ACTCCATCTGGTGTAGCAGAGCAGCGCACAGCGCTGAGAGCGCTTCCGCTGCA 778
Db      184  ACTCCATTTGGTGAGCAGCAGAGCATGGGAATAACGCTCTGGATAGCGCTATCGCTCCA 243
Qy      779  TGAGCACAAGGGCCCGCTTACCTGCTCTTACGCGTCAATGGAGTGGGCAATTTTGTG 838
Db      244  TGAATGAAAGGCGCGCTTACCTCTGTTTACGCGTCAACGGCAGTGGACACTTCTGG 303
Qy      839  GGGTGGCCGAGATGAATCCCGCTGAGCTACGCGACAGTGCCTGGGGTCTGTCTCAGG 898
Db      304  CGGTAGCCGAGATGAAGTCCCGCTGAGCTACGCGACAGTGCAGGTGTCTGGTCAAG 363
Qy      899  ACAAGTGGAGGGAAGTTGATGCTCAGTGGATTTTGTTAAGGATGTACCCATTAAC 958
Db      364  ACAATGGAAGGCAAGTTTGTATGTCGGTGGCTCTGTGTCAAAGAGAGGCGCAACACC 423
Qy      959  AGTCTCCGGCACATCAGGCTGGAGAAATACACACAAACAAACCGGTCAACAACTCCCGGACA 1018
Db      424  AGCTGATGCGCAGAGGGGTGGAGCGGACACAGACACCGCGCGGCGAGGAGCG 483
Qy      1019  CCCAGGAGTGCCTTA 1035
Db      484  CGCAGGAGTGCCTTA 500

RESULT 54
AW766493/c
LOCUS
DEFINITION
  da63c02.x1 Harland stage 19-23 Xenopus laevis cDNA clone
  IMAGE:3199586 3' similar to TR:064526 O64526 YUP8H12R.13 PROTEIN.
  ; mRNA sequence.
ACCESSION
  AW766493.1 GI:7698483
VERSION
  EST.
KEYWORDS
  African clawed frog.
SOURCE
  Xenopus laevis
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
    Xenopodinae; Xenopus.
REFERENCE
  Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
  Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
  ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
  Waterston,R. and Wilson,R.
  WashU Xenopus EST project, 1999
  Unpublished (1999)
  Other ESTs: da63c02.v1
CONTACT: Sandy Clifton, Ph.D.
  WashU Xenopus EST project, 1999
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@wustl.edu
  Library constructed by R. Harland, PhD.(University of California,
  Berkeley)
  Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: Xenopus clones from this library are available
  through the I.M.A.G.E. Consortium/INL at:
  image.llnl.gov/image/html/iresources.shtml
  Seq primer: -40UP from Gibco
  High quality sequence stop: 404.

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FEATURES
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      /clone="IMAGE:3199586"
      /clone_lib="Harland stage 19-23"
      /tissue_type="neurula"
      /dev_stage="stage 19-23"
      /lab_host="DH10B (phage-resistant)"
      /note="Vector: pCG107 (custom); Site 1: NotI; Site 2: SalI
      ; cDNA made by oligo-dT priming. Library constructed by
      Dr. Francesca Mariani in the laboratory of R. Harland,
      Ph.D. (University of California, Berkeley). References:
      xBp-2 is a transcriptional repressor that converts
      ectoderm into neural tissue. Mariani, F.V. Harland, R.M.,
      95030283. Use of large-scale expression cloning screens in
      the xenopus laevis tadpole to identify gene function.
      Grammer TC, Liu KJ, Mariani FV, Harland RM, Dev Biol.
      2000 Dec 15;228(2):197-210. PMID: 11112324; UI: 20564075;
      Note: This is a Xenopus Gene Collection (XGC) library."
BASE COUNT      146 a      147 c      127 g      168 t      4 others
ORIGIN
  Query Match      15.0%; Score 304.4; DB 2; Length 592;
  Best Local Similarity 79.4%; Pred. No. 7.2e-67;
  Matches 370; Conservative 0; Mismatches 95; Indels 1; Gaps 1;
  QY      691  GAGGAGCAGATCCACCGCTCCATTAAAGTACTCTGTTAGTACGAGCAGGCAAC 750
  Db      586  GAGCATGATATCTGCTTCCATTAAATATTTATGTGGTGTAGTAGATGGGAT 527
  QY      751  AAGCGCTGGACAGCGCTTCCGCTGATGAGCAGCAAGGGGCGCTCTACCTGCTTC 810
  Db      526  ACATGCTTGGATTAACGTTTTTTCGCTCTATGAATGGTAAAGGCGCGCTTACTTCTTC 467
  QY      811  AGCGTCAATGGGAGTGGGCATTTTGTGGGTGGCCGAGATGAAGTCCCGCTGGACTAC 870
  Db      466  AGCGTCAATGGCAGTGGATATTTCTGTGGCGTAGCTGAGATGAAGTCTCTGTGGACTAT 407
  QY      871  GGACACAGTCCCGGGTGTGCTCTCAGGCAAGTGGAAAGGGAGTTTGTATGTCCAGTGG 930
  Db      406  GGACACAGTCCCGGGTGTGCTCAGGCAAGTGGAAAGGGAGTTTGTATGTCCAGTGG 347
  QY      931  ATTTTGTTAAGGATGTACCCAAATACCAAGCTCCGGCAGATCAGGCTGGAGATAACGAC 990
  Db      346  CTTTTTGTCAAGGAGCTTCCCAACACAGCTCAGGCACATCCGCTGGAGATAACGAC 287
  QY      991  AACAAACCGGTCAAACTCCCGGACACCCAGGAGTGCCCTTAGAAAAGCCAAAGCAA 1050
  Db      286  AACAAACCGGTCAAACTCCCGGACACCCAGGAGTGCCCTTAGAAAAGCCAAAGCAA 227
  QY      1051  GTGCTGAAATTTATCAGTCTTCAACAGCAGCAACCTCCATCTTTCGACGACTTTGCTCAC 1110
  Db      226  GTGCTTAAATTCATTCGCCACTTAAAGCAGCACGACCTCCATCTTTGATGACTTTTCTCAT 167
  QY      1111  TAGGAGAAGGCCCA-GAGGAGGAGGAGTGGTGGCAAGGAAAGCGC 1155
  Db      166  TAGGAGAAGGCCGAGGAGGAGGAGGAGTGGTGGCAAGGTAACGC 121

RESULT 55
AJ453895
LOCUS
DEFINITION
  AJ453895 riken1 Gallus gallus cDNA clone 35o2r1, mRNA sequence.
ACCESSION
  AJ453895
VERSION
  AJ453895.1 GI:20263991
KEYWORDS
  chicken.
SOURCE
  Gallus gallus
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
    Phasianinae; Gallus.

```



```

REFERENCE 1 (bases 1 to 732)
AUTHORS Buerstedde, J.M.
TITLE Gallus gallus bursal lymphocyte EST
JOURNAL Unpublished (2002)
COMMENT Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES             source
    source            1..732
                        /organism="Gallus gallus"
                        /db_xref="caxon:9031"
                        /clone_lib="3502r1"
                        /cell_type="bursal lymphocyte"
                        /dev_stage="2-3 weeks old"
                        /note="CB inbred strain"

BASE COUNT  201 a   173 c   168 g   190 t
ORIGIN
Query Match      14.9%;   Score 301.8;   DB 1;   Length 732;
Best Local Similarity 82.7%;   Pred. No. 3.5e-66;
Matches 345;   Conservative 0;   Mismatches 72;   Indels 0;   Gaps 0;

Qy  1  CAAAGGCAAGATAATAAGTACAAAATGGTTGGTTACATCAGAAGGATACAGTTCAATG 60
Db  100 CGAAAGGACAGGATAATAAGTACAAAATGGTTGGTTACATCAAAGGATACAGTTCAAG 159
Qy  61  ACAATGACTTTGAGCCCTACCTTACTTGACAGTCAAAATCAGATGTAACAGTTACCCCTCAA 120
Db  160 ACAACGATTTTGAACCTTACCTTTCTGGGGAGTCAAAATCAGAACAGTATGATCCATCAA 219
Qy  121 TGAGCGACCCCTACCTGTCCAGCTATTACCCGCGTCCATTTGGATTTCTTACTCCCTCA 180
Db  220 TGACTGATCCTTTATCTGTCAAGTTATTATCCACATCTATCGGGTTTCCCTACTCTCTCA 279
Qy  181 ATGAGGCTCCGTGGTCTACTCAGGGGACCCCTCCGATTCCATACCTCACCACCTACGGAC 240
Db  280 GTGAAGCGCCATGGTCTACAGGAGGAGATCCTCCTATCCGATCTCACCACCTATGGAC 339
Qy  241 AGCTCAGTAACGGAGACCATCATTTTATGACGATGCTGTTTGGGAGGCTCGGGGCC 300
Db  340 AGCTCAGTAATGGAGATCATCATTTATGCGATGATGCTGTTTGGACAGGCTCGGGGTC 399
Qy  301 TGGGGAACAACATCTATCAGCACAGGTTCAATTTTTCCCTGAAACCTCGTTCTCAG 360
Db  400 TGGGAAATTAATATCTATCAACACCGGTTAACTTTTCCCTGAAATCCTGCTTCTCAG 459
Qy  361 CATGGGGACAAGTGGGCTCAAGGTCAGCAGACCCAGAGCTCAGCCCTCTCCCGACA 417
Db  460 CTTGGGGAACAAGTGGATCCCAAGACAGCAGACTCAAAGTTACGATATGGGAGCA 516

RESULT 56
AA099707
LOCUS
DEFINITION ZR86a12.r1 Soares pregnant_uterus_NbHPU Homo sapiens cDNA clone
IMAGE:489694 5', mRNA sequence.
AA099707
ACCESSION
VERSION
KEYWORDS
SOURCE
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 421)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaudo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins
, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.

```

<p>Generation and analysis of 280,000 human expressed sequence tags</p> <p>Genome Res. 6 (9), 807-828 (1996)</p> <p>9704478</p> <p>Contact: Wilson RK</p> <p>Washington University School of Medicine</p> <p>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108</p> <p>Tel: 314 286 1800</p> <p>Fax: 314 286 1810</p> <p>Email: estowatson.wustl.edu</p> <p>This clone is available royalty-free through LLNL ; contact the</p> <p>IMAGE Consortium (info@image.llnl.gov) for further information.</p> <p>Insert Length: 811 Std Error: 0.00</p> <p>Seq primer: -28M13 rev2 from Amersham</p> <p>High quality sequence stop: 360.</p>	
<p>FEATURES</p>	<p>Location/Qualifiers</p> <p>1..421</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="GDB:3804281"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="IMAGE:489694"</p> <p>/clone_lib="Soares_pregnant_uterus_NbHPU"</p> <p>/sex="female"</p> <p>/dev_stage="adult"</p> <p>/lab_host="DH108"</p> <p>/note="Organ: uterus; Vector: pPT73-Pac; Site 1: Not I; Site 2: Eco RI; left strand cDNA was primed with a Not I oligo(dT) primer [5', AACTGGAAGAAATTCGGCGCGCCGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pPT73 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."</p>
<p>BASE COUNT</p>	<p>97 a 70 c 156 t 4 others</p>
<p>ORIGIN</p>	<p>Query Match 14.8%; Score 300.4; DB 1; Length 421;</p> <p>Best Local Similarity 98.2%; Pred. No. 6.9e-66;</p> <p>Matches 323; Conservative 0; Mismatches 4; Indels 2; Gaps 2;</p>
<p>Qy 1700</p>	<p>CTGCTAGACAGATAACCTTTAAATTTTTCACAAATTTGGCAGACACATTTTTTTTTTTTGA 1759</p> <p>     </p>
<p>Db 1</p>	<p>CTGCTAGACAGATAACCTTTAAATTTTTCACAAATTTGGCAGACAC-TTTTTTTTTTTTGA 59</p> <p>     </p>
<p>Qy 1760</p>	<p>AAATCTTTTCCTTCAGATCTCTGCCCACTGAACAGCCACCGTCCCTCACTGCTCGGT 1819</p> <p>     </p>
<p>Db 60</p>	<p>AAATCTTNCCTTCAGATCTGTGCGCCACTGAACAGCCACCGTCCCTCACTGCTCGGT 119</p> <p>     </p>
<p>Qy 1820</p>	<p>GTCCGATGGCGCTCGATGGTTGGGGCATGATGTGTGAGAGAACTGGAAGGTGCTTTAG 1879</p> <p>     </p>
<p>Db 120</p>	<p>GTCCGATGGCGCTCGATGGTTGGGGCATGATGTGTGAGAGAACTGGAAGGTGCTTTAG 179</p> <p>     </p>
<p>Qy 1880</p>	<p>GTCTGGTTCAGGTCGGGCATCTTTGTTGTCACATCTTTTAAATTTTACACCTTT 1939</p> <p>     </p>
<p>Db 180</p>	<p>GTCTGGTTCAGGTCGGGCATCTTTGTTGTCACATCTTTTAAATTTTACACCTTT 239</p> <p>     </p>
<p>Qy 1940</p>	<p>TCTTAAGAATTTCTAATGCGGCTTAAAGTTTATATACCAATAATGCTGAGCTTTAAGTGT- 1998</p> <p>     </p>
<p>Db 240</p>	<p>TCTTAAGAATTTCTAATGCGGCTTAAAGTTTATATACCAATAATGCTGAGCTTTAAGTGT- 299</p> <p>     </p>
<p>Qy 1999</p>	<p>AGGATCTGGTAGTACAGACACTGTGATGG 2027</p> <p>     </p>
<p>Db 300</p>	<p>AGGATCTGGTAGTACAGACACTGTGATGG 328</p> <p>     </p>
<p>RESULT 57</p>	<p>741 bp mRNA linear EST 25-JAN-2001</p>
<p>AJ397688</p>	<p>LOCUS AJ397688 dkfz426 Gallus gallus cDNA clone 30j10r1, mRNA sequence.</p>
<p>DEFINITION</p>	<p>Accession</p>
<p>ACCESSION</p>	<p>Version</p>
<p>VERSION</p>	<p>Keywords</p>
<p>KEYWORDS</p>	<p>EST.</p>
<p>SOURCE</p>	<p>chicken.</p>

```
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 741)
AUTHORS Abdrakhmanov,I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy
,J., Korn,B. and Buerstedde,J.M.
TITLE A large database of chicken boreal ESTs as a resource for the
analysis of vertebrate gene function
JOURNAL Genome Res. 10 (12), 2062-2069 (2000)
MEDLINE 20568495
COMMENT Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institut
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES
Source
1..741
/organism="Gallus gallus"
/strain="CB"
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/clone_lib="dkf426"
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/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
BASE COUNT 241 a 165 c 182 g 153 t
ORIGIN
Query Match 14.8%; Score 300.2; DB 1; Length 741;
Best Local Similarity 76.9%; Pred. No. 9e-66;
Matches 379; Conservative 0; Mismatches 113; Indels 1; Gaps 1;

Qy 693 GGAGGACATCCACCGCTCCATTAGTACTCCATCTGCTGTAGCAGACGACGCGCAAA 752
Db 1 GGAGGATATCCACCGCTCCATTAAATCAACATCTGTGCGAGTAGCAGCAGCGCAAA 60

Qy 753 GCGCCTTGACAGCGCTTCGCTGCATGAGCAGCAAGGGCGCGTCTACCTGCTCTTCAG 812
Db 61 GAGACTGGATGCGCGCTACCGCTCCATGAATGGGAGGGCGCGTTTACTTACTGTTTCAG 120

Qy 813 CGTCAATGGAGTGCGGATTTTGTGGGTGGCGGAGATGAAGTCCCGCTGGACTACGG 872
Db 121 TGTCAACGGTAGCGGTCACTTCTCGGAGTAGCAGAAATGAAATCTGCTGTGGACTCAA 180

Qy 873 CACAGTCCGGGTCTGGTCTCAGGACAGTGAAGGGGAAGTTTCATGTCCAGTGGAT 932
Db 181 CAGGTGCGGGTGTGGTCCCGAGGACAGTGAAGGAGCGTTTGTATGTCAAGTGGAT 240

Qy 933 TTTTGTAAAGGATATACCAATACCAAGCTCCGACATCAGGCTGGAGAAATACGACAA 992
Db 241 TTTTGTAAAGGACGTTCCCAACACCGAGCTCGGACATCGCCTAGACACAGGAA 300

Qy 993 CAACCGGTCAAACTCCCGGGACACCCAGGAGTGCGCTTGAAGAAAGCAAGCAAGT 1052
Db 301 TAAACAGTGACCAACTCCAGGACACTCAGGAGTGCGCTCTGAAAAGGCTAAGCAGGT 360

Qy 1053 GCTGAAATATCAGTTCTTACAGCAGCAGCACTCCATCTTCGACGACTTGTCTACTA 1112
Db 361 GTTGAATATCATTCGCCACCTACAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420

Qy 1113 CGAAGCGGCA - GAGGAGGAGGAGGTGGTGGCGCAAGGACCGGAGAGTGGAAACA 1171
Db 421 TGAGAAAGCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480

Qy 1172 ATGAGGCGGAAC 1184
Db 481 GAAGGCGCATCCC 493

RESULT 58
AI604044
LOCUS
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## DEFINITION

vr18d03.y1 Barstead mouse myotubes MPURB5 Mus musculus cDNA clone

IMAGE:1120997 5', mRNA sequence.

AI604044

VERSION AI604044.1 GI:4613206

EST.

house mouse.

Mus musculus

ORGANISM

REFERENCE

1 (bases 1 to 487)

AUTHORS

Marta,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person

,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter

,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

COMMENT

Contact: Marra MYWashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LML ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:610333

This read is a RESEQUENCE of a previously sequenced mouse clone

correct orientation

Seq primer: -40RP from Gibco

High quality sequence stop: 470.

Location/Qualifiers

1..487

/organism="Mus musculus"

/strain="C3H"

/db\_xref="taxon:10090"

/clone="IMAGE:1120997"

/cell\_line="Barstead mouse myotubes MPURB5"

/lab\_host="DH10B"

/notes="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site\_1: EcoRI; Site\_2: NotI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TGTTAGCAATCTGAAGTGGGAGCGCGCTTTTTTTTTTTTTTTTTT

3']; double-stranded cDNA was ligated to Eco RI adaptors

[AATCGGATCTTG], digested with Not I and cloned into the

Not I and Eco RI sites of the modified pT73 vector.

Library constructed by Bob Barstead. The C2C12 cell line

(available from ATCC, catalog # CRL-1772) differentiates

rapidly, forming contractile myotubes and producing

characteristic muscle proteins."

BASE COUNT 114 a 143 c 117 g 113 t

ORIGIN

Query Match 14.8%; Score 300; DB 1; Length 487;

Best Local Similarity 89.0%; Pred. No. 9.1e-66;

Matches 324; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 1 CAAAGGACGAAGATAAAGTACAAATGGTTCGTATCATCAGAGATACAGTTTCATG 60

Db 124 CAAAGGACGAAGATAAAGTACAAATGGTTCGTTCGATCAGAGATACAGTTTCATG 183

Qy 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATACAGAGTAACAGTTACCCCTCAA 120

Db 184 ACAATGACTTTGAGCCCTACCTTCTGGACAGTCCAAATCCAGATTAACAGTTACCCCTCGA 243

Qy 121 TGAGCGACCCCTACCTGTCCAGCTATTACCCGCCGCTCCATTGGATTTCCTTACTCCCTCA 180

Db 244 TGAGTGATCCTTACCTGTCCAGTTACTATCCACCATCCATTGGATTTCCTTACTCCCTCA 303

Qy 181 ATGAGGCTCCGTGGTCTACTGCGAGGGACCCCTCCGATTCATACCTCACCACCTACCGAC 240

Db 304 GCGAGGACCATGGTCCACTGCGAGGGGACCCCTCCCATCCCGTATCTCATCTACCTATGGAC 363

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QY 241 AGCTCAGTAACGAGACCATCTATTTTATGACGATGCTGTTTTTGGGCGACCTGGGGGCC 300
Db 364 AACTTAGTAATGAGACCATCACTTCATGCATGATGCTGTGTTGGGCGACCTGGGGTC 423
QY 301 TGGGGAACAACATCTATCAGCAGCAGGTTCAAATTTTCCCTGAAACCCCTGGTTCAG 360
Db 424 TGGGGAACAACATTTTACCAGCAGCGTTTAAATTTTCCCTGAAACCCCTGCATTTCTAG 483
QY 361 CATG 364
Db 484 CATG 487

RESULT 59
LOCUS BE540016 752 bp mRNA linear EST 09-AUG-2000
DEFINITION 601060774F2 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447139 5',
mRNA sequence.
ACCESSION BE540016
VERSION BE540016.1 GI:9768661
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 752)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM8420 row: d column: 20
High quality sequence stop: 626.
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        /cell_line="MGC36"
        /lab_host="DH10B"
        /note="Organ: Cervix; Vector: pCMV-SPORT6; Site 1: NotI;
        Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
        Average insert size 1.5 kb. Library prepared by Life
        Technologies."
BASE COUNT 211 a 163 c 197 g 181 t
ORIGIN
Query Match 14.7%; Score 298.4; DB 2; Length 752;
Best Local Similarity 73.6%; Pred. No. 2.6e-65;
Matches 434; Conservative 0; Mismatches 151; Indels 5; Gaps 4;

QY 583 GAATCCACCCCGCTCTGTAAGAACTGAAGCGCTGCTCACAGCTACACCCGGAAGAGTTT 642
Db 83 GAACCCACCCAGGTGTTGGAGAGCTTCGGTCCATTAACTAATACCCCAAGATTTT 142
QY 643 GAGTGAATCTGAAAGCGGGCGGTGTTTCATCATCAAGAGCTACTCTGAGGACGATC 702
Db 143 GACTGGAATCTGAAACATGCGCGGGTTTTCATCATTAAGAGCTACTCTGAGGACGAT 202
QY 703 CACCGCTCCATTAGTACTCCATCTGCTGTAGCAGCAGCAGCAACAGCCCTGGAC 762
Db 203 CACCGTTCCATTAAGTATAATATTGTCGAGCAGCAGCATGTTAACAAGAGACTGAT 262
QY 763 AGGCGCTTCGCTGCATGAGCAGCAAGGGGCGCGCTCTACCTGCTCTTCAGCGTCAATGGG 822
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Db 263 GCTGCTTATCGTTCATGAACGGGAAGGCCCGCTTTTACTTACTTTTTCAGTGTCAACGCG 322
QY 823 AGTGGGCAATTTTGTGGGGTGGCCGAGATGAAGTCCCGCTGGGACTACGGCACCACTGCC 882
Db 323 AGTGACACTTCTGTGGGCTGGCAGAAATGAATCTCTGTGGACTACAACACATGTGCA 382
QY 883 GGGGCTCTGCTCAGGACAAGTGGGAAGGGGAAGTTTGTATGTCCAGTGGATTTTGTGAAG 942
Db 383 GGTGTGTGCTCCAGGACAAATGGAA-GGGTCTGTTTGTATGTCTCAGGTGGA-TTTTGTGAAG 440
QY 943 GATGTACCCCAATTAACCACTCCGCGACATCAGGCTGGAGATAAAGCAACAAACCGGTC 1002
Db 441 GACGTTCCCAATAGCCAACTCGGACACATTTGCTTAGAAGAACAGAAATTAACAGTGTG 500
QY 1003 ACAAACTCCCGGGAACACAGGAGTGCCTTTAGAAAAAGCCAAAGTGTGTAATAAT 1062
Db 501 ACCAACTTAGGACACTCAGGAAGTGCCTCTGGAAAAAGGCTA--GCAGGTGTGAATAAT 558
QY 1063 ATCAGTTCTTACAAGCACAACCTCCATCTTCGAGAGCTTTTGTCTCACTACGAGAAGCGC 1122
Db 559 ATAGCCAGCTACAGCACACCACTTTCCAT-TTTGATGACTTCTCACAATATGAGAACGC 617
QY 1123 CAGAGGAGGAGGAGTGTGCGCAAGGAACGCGCAGAGTCGAACAAACAA 1172
Db 618 CAGAGGAAGAAGAAAGTGTTAACAGGACGCTCAGGTCCGTGGGAATTA 667

RESULT 60
LOCUS ALS84855 630 bp mRNA linear EST 28-FEB-2001
DEFINITION ALS84855 Stratagene Chick Embryo Lambda cDNA Library (* 937405)
Gallus gallus cDNA clone ROS015C08, mRNA sequence.
ACCESSION ALS84855
VERSION ALS84855.1 GI:13163588
KEYWORDS EST.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 630)
AUTHORS Murray, F.
TITLE Stratagene Chick Embryo Lambda cDNA Library
JOURNAL Unpublished (2001)
COMMENT Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbserc.ac.uk
Seq primer: T3
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    1..630
        /organism="Gallus gallus"
        /db_xref="taxon:9031"
        /clone="ROS015C08"
        /clone_lib="Stratagene Chick Embryo Lambda cDNA Library (*
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        /tissue_type="Embryo"
        /dev_stage="5 days old"
        /lab_host="SOLR cells (kanamycin resistant)"
        /note="Vector: pBLUESCRIPT SK; Site 1: EcoRI; Site 2: XhoI
        ; Cloned unidirectionally. Primer: Oligo dT. Uni-ZAP XR
        vector. Average insert size: 1.5kb.; 5' adaptor sequence:
        5' GAATTCGGCAGCAG 3'; 3' adaptor sequence: 5'
        CTCGAGTTTTTTTTTTTTTT 3'."
BASE COUNT 201 a 116 c 142 g 169 t 2 others
ORIGIN
Query Match 14.7%; Score 298.2; DB 1; Length 630;
Best Local Similarity 75.5%; Pred. No. 2.8e-65;
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Matches 383; Conservative 0; Mismatches 123; Indels 1; Gaps 1;
QY 667 GTGTTTCATCATCAAGAGCTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCCATC 726
Db 15 GTGTTTATAATCAAAAGTTATTAGAGGACGATATTCATCGCTCCATTAAGTACTCTATC 74
QY 727 TGTGTAGCAGACAGCGGCAACAAAGCGCTGACAGCGCTTCCGCTGATGAGCAGC 786
Db 75 TGTGTGTAGTACTGAACATGTTAAAGCGCTTGGATGCTGTACCGTTCCTTGAATGGA 134
QY 787 AAGGGCGCGTCTACCTGCTCTTCAGCGTCAATGSGAGTGGGCAATTTTGTGGGGTGGCC 846
Db 135 AAAGCGCGCTCTATTACTCTTCAGTGTGAATGCGAGTGACACTTTTGTGGAGTGGCT 194
QY 847 GAGATGAAGTCCCCCGTGGACTACGGCAACAGTGCAGCGGTCTGCTCAGGACAAGTGG 906
Db 195 GAGATGAAGTCTGTGTGGACTACAATGTCATATGCTGCGCTGCTGCTCAGGATAAGTGG 254
QY 907 AAGGGGAAGTTTGATGTCAGTGAATTTTGTGAAGGATGACCAATTAACGAGCTCGG 966
Db 255 AAGGGCAAGTTTGATGTCAAATGGAATCTTTGTCAAGACGTTTCCCAATAACCAACTCGG 314
QY 967 CACATCAGGCTGGAGATAACGACAAACAAACCGGTCAACAATTCAGTCTCAAGCACACAAC 1026
Db 315 CATATTCGTTGGAAACAATGACAAACAAACAGTTACCAATTCGAGGGACACTCAAGAA 374
QY 1027 GTGCCCTTAGAAAAAGCAAGCAAGTGTGAAAAATTCAGTCTCAAGCACACAAC 1086
Db 375 GTACCCCTAGAAAAAGCAAGCAAGTGTGAAAAATTCAGTCTCAAGCACACAAC 434
QY 1087 TCCATCTTCAGCAGCTTTGCTCAGTACGAGAAAGCG-CCAGAGGAGGAGGAGTGGTGGC 1145
Db 435 TCAATCTTCATGACTTTGTCATATTATGAAAGCGTCAAGAAAGGAGGAGGAGGATCGT 494
QY 1146 AAGGAGCGGAGCTCGAACAACAA 1172
Db 495 AGGAGGAGGAGTAAACAACAATAA 521

RESULT 61
BE375521
LOCUS
DEFINITION
601225407F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3584040 5',
mRNA sequence.
BE375521
ACCESSION
VERSION
BE375521.1 GI:9320886
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 612)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-x@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8741 row: m column: 01
High quality sequence stop: 590.
Location/Qualifiers
1. 612
/organism="Mus musculus"
/strain="FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:3584040"
/clone_lib="NCI_CGAP_Mam1"

FEATURES
source
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/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sali;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 204 a 107 c 135 g 166 t
ORIGIN
Query Match 14.6%; Score 295.8; DB 2; Length 612;
Best Local Similarity 70.8%; Pred. No. 1.1e-64;
Matches 407; Conservative 0; Mismatches 167; Indels 1; Gaps 1;
QY 620 ACAGCTACAAACCCGAAAGAGTTTGAAGTGAATCTGAAAGCGGCGTGTGTTTCATCATCA 679
Db 1 ACAATTATATCCCAAGACTTTGATTGGAACCTGAAGAATGGACGTGTGTTTATATTA 60
QY 680 AGAGCTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCTGCTGTGTAGCAGACAG 739
Db 61 AGAGCTATTCTGAGGATGATATACATCGTTCCATCAAGTACTCTATCTGTGTAGTACTG 120
QY 740 AGCAGCGACACAGCGCTCGACAGCGCTTCCGCTGCATGAGCAGCAAGGGCGCCGCTCT 799
Db 121 AGCATGTTAATAAGCGTTTGGATGCACTTATCGTTCCCTGGAATGGGAAAGGCCACTCT 180
QY 800 ACCTGCTCTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGGTGGCCGAGATGAAGTCCC 859
Db 181 ATTACTCTTCAGTGTGAATGGCAGTGGACATTTTGTGGAGTGGCTGGAATGAAGTCTG 240
QY 860 CCGTGGACTACGGCACAGTGCAGCGGCTGTGGTCTCAGGACAAAGTGGAAAGGGAAGTTTG 919
Db 241 TTGTAGACTATAATGCTTATGCTGCTGTGCTCAGGATAAGTGGAGGCAAAATTTG 300
QY 920 ATGTCAGTGGATTTTGTAAAGATGTACCCAAATACAGAGTCCGCGCACATCAGGCTGG 979
Db 301 AAGTTAAATGGATCTTTGTCAAAAGATGTTCCCAATAACCAATTAACGACATATTGCGT 360
QY 980 AGAATAACGACAAACAAACCGGTCAAAATCCCGGACACCCAGGAGGTGCCCTTAGAAA 1039
Db 361 AAAATAATGACAAACCAACAGTAACCAATTCAGGGACATCTCAAGAGTACCCCTAGAAA 420
QY 1040 AAGCAAGCAAGTGTGAAATTAATATCAGTTTC-CTAAGACACACAACTCCATCTTCGAC 1098
Db 421 AAGCAAGCAAGTGTGTTAAATAATGCTACTTTTCAAGCATACCACTCAATCTTTGAT 480
QY 1099 GACTTTGCTCACTACGAGAGCGCCAGAGGAGGAGGAGTGGTGGCGCAAGGACGGCAGA 1158
Db 481 GACTTGCACATTAATGAAAGCGTCAAGAGAGGAGGAGGAGCCATGCGAAGGAGAGACATA 540
QY 1159 GTCMAAACAAACATAGAGGCGCAACCAAGTTTCTTA 1193
Db 541 GAAACAAGCAATAACCAACCGTGTGGAGATGTCCTA 575

RESULT 62
BB654392
LOCUS
DEFINITION
BB654392 RIKEN full-length enriched, 2 days neonate thymus thymic
cells Mus musculus cDNA clone C920004N12 5', mRNA sequence.
BB654392
ACCESSION
VERSION
BB654392.1 GI:16488220
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 637)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hasegawa, T., Hara, A.,
Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okada
Okazaki, Y., Okido, T., Saito, K., Sakai, C., Sakai, K., Sano, H., Sasaki
D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
```

Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
Unpublished (2001)

## JOURNAL

## COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suihoro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/

Carninci, P., Shibata, Y., Hayashizaki, Y., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, K., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.  
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)

Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

## FEATURES

## source

Location/Qualifiers

1. 637

/organism="Mus musculus"

/strain="C57BL/6J"

/db.xref="taxon:10090"

/clone="C920004N12"

/clone.lib="RIKEN full-length enriched, 2 days neonate

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/dev\_stage="2 days neonate"

/note="Vector: pSPOT1, Site 1: SalI; Site 2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)

)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, *Proc. Natl. Acad. Sci. U S A*, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, *Development*, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, *Hum Mol Genet* 7: 1967-1978."

Mol Genet 7: 1967-1978."

121 a 210 C 170 G 136 T

BASE COUNT 121 a 210 C 170 G 136 T

## ORIGIN

Query Match 14.5%; Score 294.2; DB 2; Length 637;  
Best Local Similarity 89.4%; Pred. No. 2.9e-64;

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Qy	61	ACAATGACTTTGAGCCCTACCTTACTGACAGATCAATACAGTAACAGTTACCCCTCAA	120						
Db	331	ACAATGACTTTGAGCCCTACCTTACTGACAGATCAATACAGTAACAGTTACCCCTCGA	390						
Qy	121	TGAGCGACCCCTACTGTCACAGTATTACCCGCGCTCCATTGGATTTCCTTACTCCCTCA	180						
Db	391	TOAGTGATCTCTTACTGTCAGTACTATCCACCATCCATTGGATTTCCTTACTCCCTCA	450						
Qy	181	ATGAGGCTCCGTCGTTACTGACGGGACCCCTCCGATTCCATACCTACACGAC	240						
Db	451	CGAGGACCATGTCCTACTGACGGGACCCCTCCCATCCGTCATCTACTACCTATGGAC	510						
Qy	241	AGCTCAGTAACGGAGACCATCATTTTATGACGAGTCGTTTGGGAGCCTGGGGGCC	300						
Db	511	AACTTAGTAATGGAGACCATCATTTTATGACGAGTCGTTTGGGAGCCTGGGGGCC	570						
Qy	301	TGGGGAACCAATCTATCAGCACAGG-TTCAATTTTTTCCCTGAAAAACCTCGCTTCTCA	359						
Db	571	TGGGGAACCAATCTATCAGCACAGGTTTATTTTTTCCCTGAAAAACCTCGCTTCTCA	630						
Qy	360	GCATGGG 366							
Db	631	GCATGGG 637							
RESULT 63	AA323869	316 bp	mrna	linear	EST 20-APR-1997				
LOCUS	AA323869	316 bp	mrna	linear	EST 20-APR-1997				
DEFINITION	EST26711 Cerebellum II Homo sapiens cDNA 5' end, mRNA sequence.								
ACCESSION	AA323869								
VERSION	AA323869.1	GI:1976196							
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
	1. (bases 1 to 316)								
	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult								
	C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White								
	O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,								
	Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald								
	L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S., Glodek, A.,								
	Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkie, P.S., Jr., Kelley, J.M.,								
	Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,								
	Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,								
	Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R.,								
	Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,								
	Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,								
	Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,								
	Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,								
	Kunsch, C., Hung, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L.,								
	Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon								
	M.R., Rosen, C.A., Hasseltine, W.A., Fields, C., Fraser, C.M. and								
	Venter, J.C.								
TITLE	Initial assessment of human gene diversity and expression patterns								
JOURNAL	based upon 83 million nucleotides of cDNA sequence								
MEDLINE	Nature 377 (6547 Suppl), 3-174 (1995)								
COMMENT	96026280								
	Other ESTs: THC192215								
	Contact: Kerlavage, AR								
	Bioinformatics								
	The Institute for Genomic Research								
	9712 Medical Center Drive, Rockville, MD 20850 USA								
	Tel: 3018699056								
	Fax: 3018699423								
	Email: arkerlav@tigr.org								
	For clone availability, additional sequence and expression								

information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.

## FEATURES

Location/Qualifiers  
1..316

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/db\_xref="taxon:9606"  
/clone\_lib="Cerebellum II"  
/tissue\_type="cerebellum"  
/dev\_stage="adult"  
/notes="Organ: brain; Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI"  
EcoRI; Site\_2: XhoI

BASE COUNT 88 a 80 c 87 g 56 t 5 others  
ORIGIN

Query Match 14.2%; Score 287.2; DB 1; Length 316;  
Best Local Similarity 97.1%; Pred. No. 1.5e-62;  
Matches 300; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 851 TGAAGTCCCGCTGAGTACGGCACCACTGCGGGGTCTGCTCTCAGGACAAGTGGGAAGG 910  
Db 8 TGAAGTCCCGCTGAGTACGGCACCACTGCGGGGTCTGCTCTCAGGACAAGTGGGAAGG 67

QY 911 GGAAGTTTGATGTCAGTGGATTTTCTTAAGGATGTACCAATPAACCAAGCTCCGGCACA 970  
Db 68 GGAAGTTTGATGTCAGTGGATTTTCTTAAGGATGTACCAATPAACCAAGCTCCGGCACA 127

QY 971 TCAGGCTGGAGATTAAGCACACAAACGGGTCAAACTCCGGGACACCCAGGAGTGC 1030  
Db 128 TCAGGCTGGAGATTAAGCACACAAACGGGTCAAACTCCGGGACACCCAGGAGTGC 187

QY 1031 CTTTAAAAAGCCCAAGCAAGTGTGAAATTTATCAGTTCTACAGCACACACACCTCCA 1090  
Db 188 CTTTAAAAAGCCCAAGCAAGTGTGAAATTTATCAGTTCTACAGCACACACACCTCCA 247

QY 1091 TCTTCGACGACTTTGCTCCTACAGAGAGGCCCA-GAGGAGGAGGAGTGTGTGCGCAAGG 1149  
Db 248 TCTTCGACGACTTTGCTCCTACAGAGAGGCCCAAGGAGGAGTGTGTGTGCGCAAGG 307

QY 1150 AACGGCAGA 1158  
Db 308 AACGGCAGA 316

## RESULT 64

AJ447891  
LOCUS AJ447891 riken1 Gallus gallus cDNA clone 18a13r1, mRNA EST 19-APR-2002  
DEFINITION AJ447891  
ACCESSION AJ447891  
VERSION AJ447891.1 GI:20215112  
KEYWORDS EST.  
SOURCE chicken.  
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 616)

Buerstedde, J.M.

Gallus gallus Bursal lymphocyte EST

Unpublished (2002)

Contact: Buerstedde JM

Cellular Immunology

Heinrich-Pette-Institute

Martinstr. 52, 20251 Hamburg, Germany

Email: URL: <http://genetics.hpi.uni-hamburg.de/dt40est.html>.

Location/Qualifiers

1..616

/organism="Gallus gallus"

/db\_xref="taxon:9031"

/clone="18a13r1"

/clone\_lib="riken1"

/cell\_type="bursal lymphocyte"

## FEATURES

source

/dev\_stage="2-3 weeks old"  
/note="CB inbred strain"

BASE COUNT 143 a 186 c 140 g 144 t 3 others  
ORIGIN

Query Match 14.0%; Score 284.8; DB 1; Length 616;  
Best Local Similarity 82.5%; Pred. No. 7.1e-62;  
Matches 325; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 CAAAGGACAGGATAATTAAGTCAAAATGGTTTCGTACATCAGAGGATACAGTTTCATG 60  
Db 196 CGAAGGACAGGATAATTAAGTCAAAATGGTTTCGTACATCAGAGGATACAGTTTCATG 255

QY 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATCAGAGTAAACAGTTACCCCTCAA 120  
Db 256 ACAACGATTTTGAACCTTACCTTCTGGGAGTCAATCAGACAGTAGTATCCATCA 315

QY 121 TGAGGACCCCTACCTGTCAGTATTAACCCGCGTCCATTTGATTTCTTACTCCCTCA 180  
Db 316 TGACTGATCCTTATCTGTCAAGTTATTATCCACCATCTATTGGGTTTCCCTACTCTCA 375

QY 181 ATGAGCTCGTGTCTACTGACGGGACCTCCGATTCATACCTCACCACCTACGGAC 240  
Db 376 GTGAAGCGGCATGCTTACAGGAGGATCCTCTATCCGATATCTCACCACCTATGGAC 435

QY 241 AGCTCAGTAAACGAGACCATCATTTTATGACGATGCTGTTTTGGGACGCTGGGGGCC 300  
Db 436 AGCTCAGTAAACGAGATCATTTTATGACGATGCTGTTTTGGGACGCTGGGGGCC 495

QY 301 TGGGGAAACAATCTATCAGCACAGGTTCAATTTTTTCCCTGAAAACCTTCGCTTCTCAG 360  
Db 496 TGGGAAATAATATCTATCAACACCGGTTTAACTTTTCCCTGAAAATCTTCGCTTCTCAG 555

QY 361 CATGGGGCAAGTGGTCTCAAGGTCAGCAGAC 394  
Db 556 CTTGGGGAACAAGGGATCCAGGGCNGGAAGAC 589

## RESULT 65

AJ977084/c  
LOCUS AJ977084/c

DEFINITION

Human.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 679)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: [cgepps-r@mail.nih.gov](mailto:cgepps-r@mail.nih.gov)

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/BLN at:

[www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html)

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 459.

Location/Qualifiers

1..679

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1587173"

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/clone_lib="NCI_CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/notes="Vector: pTT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pTT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
BASE COUNT      169 a 162 c 133 g 215 t
ORIGIN
Query Match      14.0%; Score 284; DB 1; Length 679;
Best Local Similarity 74.0%; Pred. No. 1.2e-61;
Matches 373; Conservative 0; Mismatches 130; Indels 1; Gaps 1;
QY 670 TTATCATCAAGAGCTACTCTGAGGAGCAGATCCACGGCTCCATTAAAGTACTCCATCTGG 729
Db 679 TTATCATTAAGAGCTACTCTGGGACGATATTTACCGTTCCTTAAGTATAATATTGG 620
QY 730 TGTAGCAGAGCAGCGCAACAGCGCTGGACAGCGCTTCGGTGCATGAGCAGCAAG 789
Db 619 TGCAGCAGGAGCATGTTACAGAGACTGGATGCTGCTTATCGTTCCATGAACGGGAAA 560
QY 790 GGGCCCGTCTACCTGCTCTTACAGCGTCAATGGGAGTGGGCAATTTTGTGGGGTGGCCGAG 849
Db 559 GGGCCCGTCTTACTTCTTCACTGTCACGGCAGTGGACATCTCTGTGGCGTGGCAGAA 500
QY 850 ATGAAGTCCCGGTGACTACGGCAGCGAGTGGCGGGTGTGFTCTCAGACAAAGTGGAA 909
Db 499 ATGAATCTGCTGTGACTACACACATGTCAGAGTGTGTGGTCCCGACGACAAATGGA 440
QY 910 GGGAGCTTTGATGTCAGTGGATTTTGTAGGAGTATCCCAATACCACTCCGGCAC 969
Db 439 GGTGCTTTGATGTCAGTGGATTTTGTAGGAGCTTCCCAATAGCAACTTGCACAC 380
QY 970 ATCAGCGTGGAGAAATACGACAAACCGGTCAACAACTCCCGGACACCCAGGAGGTG 1029
Db 379 ATTCGCTAGAGAACACGAGATTAACCGTGCACCACTCTAGGACACTCAGGAAGTG 320
QY 1030 CCTTAGAAAAAGCCAAAGCAAGTGTGTAATAATATCAGTTCTTACAGCACACAACTCC 1089
Db 319 CCTCTGAAAAAGCGTAAGCAGGTGTTGAAAAATATAGCCAGCTACACAGCACACACTTC 260
QY 1090 ATCTTCGACGACTTCTCTACTAGCAGAGCGCC-AGGAGGAGGAGGTGTGCGCAAG 1148
Db 259 ATTTTGTGACTTCTCAGCTATGAGAACGCCAAGAGAGGAAGAAAGTGTAAAAAG 200
QY 1149 GAACGGCAGAGTCGAAACAAACAA 1172
Db 199 GAACGTCAGGTCGTGGAAATAA 176
RESULT 66
AL627746
LOCUS
DEFINITION AL627746 XGC-gastrula Silurana tropicalis cDNA clone TGas025h05 5',
mRNA sequence.
ACCESSION AL627746
VERSION AL627746.1 GI:16597229
KEYWORDS EST.
SOURCE western clawed frog.
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 689)
REFERENCE
Huckle, B., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Huckle E
```

```
Sanger Centre
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TGas025h05.sp6
Sequencing_primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
Location/Qualifiers
source 1. 689
/organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TGas025h05"
/dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="Escherichia coli XL1-blue"
/notes="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."
BASE COUNT      139 a 253 c 166 g 129 t 2 others
ORIGIN
Query Match      13.6%; Score 274.8; DB 1; Length 689;
Best Local Similarity 79.4%; Pred. No. 2.6e-59;
Matches 324; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 1 CAAGAAGCAGATTAAGTACAAAATGGTTCTTATCATCAGAGGATACAGTTCAATG 60
Db 243 CAACAATGATCTTTTTCAGTTCAAAACGGATCCCTGCACCAAGGACGCGTGACG 302
QY 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAAAATCAGAGTAACAGTTCACCTCAA 120
Db 303 ATATGATCTTCGAGCAGTACCTGTGCGGACAGTCCCAATCAGAGTAACAGTACCTTCCA 362
QY 121 TGAGGACACCTTACTCTGTCAGCTATTACCGCGCTGCATTTGGATTTCTTACTCTCTCA 180
Db 363 TGACCGACCCGTACCTGTCCAGTTACTACCTCTCTTCTATCGGCTTTCCGTATTGCTCA 422
QY 181 ATGAGCTCCGTTGCTACTGTCAGGAGCCCTCCGATTCATACCTCACCACCTACGGAC 240
Db 423 GGAAGCTCTTTGGTCAACCGCGGGGACCCCGATCCGTCCTCACCCTACCGTACGGAC 482
QY 241 AGCTCAGTAACGAGACCATCAATTTATGACAGTGTCTTTTGGGAGCCTTGGGGGCC 300
Db 483 AGCTCAGCAACGAGACCACTTTCATGACAGTGTGCTTTTGGGAGCCTTGGGGGCC 542
QY 301 TGGGGAACAACTCTATCAGCAGAGTTCAATTTTTCCTGAAAACCTTGGTCTCAG 360
Db 543 TGGGGAATAACATCTATCAGCACCGGTTCACTTCTCCCGGAAAACCCAGCCTTTTCG 602
QY 361 CATGGGGAAGTGGTCTCAGGTCAGCAGACCCAGAGCTCAGCCT 408
Db 603 CATGGGGAAGTGGTCTCAGGTCAGCAGACCCAGAGCTCAGCCT 650
RESULT 67
AL398704
LOCUS
DEFINITION AL398704 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727735
3', mRNA sequence.
ACCESSION AL398704
VERSION AL398704.1 GI:2051817
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
REFERENCE
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie
```



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.TITLE      T., Waterston,R. and Wilson,R.
JOURNAL     WashU-Merck EST Project 1997
COMMENT     Unpublished (1997)
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: eet@watson.wustl.edu
            This clone is available royalty-free through LNL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 831 Std Error: 0.00
            Seq primer: -41m13 fwd. ET from Amersham
            High quality sequence stop: 436.

FEATURES
  source
    1..447
      /organism="Homo sapiens"
      /db_xref="GDB:5924646"
      /db_xref="taxon:9606"
      /clone="IMAGE:727735"
      /clone_lib="Soares_testis_NHT"
      /sex="male"
      /lab_host="DH108"
      /note="Vector: pT73D-Pac (Pharmacia) with a modified
      polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
      was prepared from mRNA obtained from Clontech Laboratories
      Inc. and primed with a Not I - oligo(dT) primer [5',
      TGTACCAATCTGAAGTGGAGCGCGGCCCAATTTTTTTTTTTT 3'].
      Double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Not I and cloned into the Not I
      and Eco RI sites of the modified pT73 vector. Library
      went through one round of normalization to Cot5, and was
      constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT  103 a 75 c 111 g 158 t
ORIGIN
Query Match      13.5%; Score 274; DB 1; Length 447;
Best Local Similarity 100.0%; Pred. No. 3,7e-59;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1755 TTTGAAATCTTCTCCAGATCTGTTGCCACTGAACGCCACCGTCCCTCACTGTC 1814
DB 1 TTTGAAATCTTCTCCAGATCTGTTGCCACTGAACGCCACCGTCCCTCACTGTC 60

QY 1815 CTGCTGTCGAGTGGTGGATGTTGGGGCATGATGTGTGGAGCACTGGAAGTGC 1874
DB 61 CTGCTGTCGAGTGGTGGATGTTGGGGCATGATGTGTGGAGCACTGGAAGTGC 120

QY 1875 TTTAGGCTGCTCAGGTCGGGCATCTTTGTTGTTTGCACATCTTTTAAATTTTACA 1934
DB 121 TTTAGGCTGCTCAGGTCGGGCATCTTTGTTGTTTGCACATCTTTTAAATTTTACA 180

QY 1935 CTTTCTTAAAGATTTCTAATGCCGCTTAAGTTTATATACCAATATAGTGCAGCTTTAA 1994
DB 181 CTTTCTTAAAGATTTCTAATGCCGCTTAAGTTTATATACCAATATAGTGCAGCTTTAA 240

QY 1995 GTGTAGGATCTGTAGTACACAGCTGTGATGA 2028
DB 241 GTGTAGGATCTGTAGTACACAGCTGTGATGA 274

RESULT 68
LOCUS      AW641341
DEFINITION cm06d01.w1 Blackshear/Soares normalized Xenopus egg library Xenopus
            laevis cDNA clone PBX0105D01 5', mRNA sequence.
ACCESSION  AW641341
VERSION     AW641341.1 GI:7398599
KEYWORDS   EST.
SOURCE     African clawed frog.
ORGANISM   Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 553)
Blackshear,P.J., Lai,W.S., Thorn,J.M., Kennington,E.A., Staffa,N.G.
Jr., Moore,D.T., Bouffard,G.G., Beckstrom-Sternberg,S.M., Touchman
J.W., Bonaldo,M.F. and Soares,M.B.
The NIHES Xenopus maternal EST project: interim analysis of the
first 13,879 ESTs from unfertilized eggs
Gene 267 (1), 71-87 (2001)
21211403
Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
USA
Tel: 919 541-4899
Fax: 919 541-4571
Email: black009@niehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
cdna@resgen.com
DNA Sequencing and analyses performed by National Institutes of
Health Intramural Sequencing Center (NISC).
PCR Primers
FORWARD: TGTAAACACGCGCCAGT
BACKWARD: CAGGAACAGCTATGACC
Plate: 0105 row: D column: 01
Seq primer: T7 primer.
Location/Qualifiers
1..553
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="PBX0105D01"
/clone_lib="Blackshear/Soares normalized Xenopus egg
library"
/sex="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH108"
/note="Vector: pT73-Pac; Site 1: EcoRI; Site 2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
pT73-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subtraction: two
approaches to facilitate gene discovery', Genome Research
6:791-806, 1996. The first strand synthesis used a
NotI-dT18 primer; double stranded cDNAs were ligated to
EcoRI adaptors, digested with NotI, and directionally
cloned into the NotI and EcoRI-digested pT73-Pac vector.
The library contained approximately 7.2 X 10^5
recombinants, with average insert sizes of 1-1.5 kb."
BASE COUNT  139 a 155 c 125 g 134 t
ORIGIN
Query Match      13.5%; Score 273; DB 2; Length 553;
Best Local Similarity 78.4%; Pred. No. 7e-59;
Matches 327; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 1 CAAAGGACAAGATAATAAGTACAAATGGTTTCGTTACATCAGAAGGATACAGTTTCATG 60
DB 33 CAAACAATGATCTTATTTTCAGTTCAAACCGATCCCTGCATCAGAAGGACAGCGTGCACG 92

QY 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAATACAGATACAGTTACCCCTCAA 120
DB 93 ATAATGACTTTGAGCAGTACCTTCGGGGCAGTCCCAATCAGATACAGTACCCCTCCA 152

QY 121 TGAGGACCCCTTACCTGTCCAGCTATTACCCGCGTCCATTGGATTTCCTTACTCCCTCA 180
DB 153 TGACAGACCCCTTATCTATCCAGTTACTACCTCTCTTATTTGGCTTTCGTTATCCCTCA 212

QY 181 ATGAGGCTCGTGGTCTACTGTCAGGGGACCCCTCCGATTTCCATACCTCACCTACGGAC 240

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Db 213 GCGAGCTCCTTGGTCAACTGGTGGGACCCCCCATTCCTTACCTCACCCTCGTAGGAC 272
QY 241 AGCTCAGTAACGAGACCATCATTTTATCAGCATGCTGTTTTGGGACGCTTGGGGCC 300
Db 273 AGCTCAGTAACGAGACCATCATTTTATCAGCATGCTGTTTTGGGACGCTTGGGGCC 332
QY 301 TGGGGAACAACATCTATCAGCAGAGTTCATTTTTCCTGAAACCCCTGGTTCAG 360
Db 333 TGGGGAATAACATTTATCAACACCGCTTCAACTTCTCCAGAAACCCAGCCTTTTCTG 392
QY 361 CATGGGGACAAGTGGTCTCAAGGTCAGCAGACCCAGAGCTCAGCTCTCCAGCA 417
Db 393 CTTGGGGACAAGTGGTCTCCAGGGCAGAGCCAGAACTCTGCTATGGGGCA 449

RESULT 69
AW420132 639 bp mRNA linear EST 09-FEB-2000
LOCUS fJbF09.y1 zebrafish gridded kidney Danio rerio cDNA 5' similar to
DEFINITION TR:064526 O64526 YUPBHL2R.13 PROTEIN. i, mRNA sequence.
ACCESSION AW420132
VERSION AW420132.1 GI:6948064
KEYWORDS EST
SOURCE zebrafish.
ORGANISM Danio rerio
REFERENCE 1 (bases 1 to 639)
AUTHORS Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrfish@watson.wustl.edu
cDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Washington University Genome Sequencing Center Clone Distribution:
Genome Systems, St. Louis, Missouri (web address:
www.genomesystems.com) (email contact: info@genomesystems.com) and
Research Genetics, Huntsville, Alabama (web address: www.resgen.com)
) (email contact: info@resgen.com) and
ResourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
www.rzpd.de)
Seq primer: T3 ET from Amersham
High quality sequence stop: 436.
Location/Qualifiers
1. .639
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="zebrafish gridded kidney"
/sex="mixed"
/tissue_type="kidney pooled from 300 wild type adults"
/lab_host="XLOLR"
/notes="Organ: kidney; Vector: pBK-CMV; Site 1: EcoRI;
Site 2: XhoI; Oligo dt cDNA library constructed from mRNA
pooled from pooled kidney tissue from 300 adult
zebrafish."
BASE COUNT 136 a 194 c 189 g 120 t
ORIGIN
Query Match 13.4%; Score 272.6; DB 2; Length 639;
Best Local Similarity 68.9%; Pred. No. 9.2e-59;
Matches 399; Conservative 0; Mismatches 159; Indels 21; Gaps 1;
QY 421 CCCCCAGCTTGGTCAACCGCAGTATCAGAGCCTCAGCAGCCACCCAGAGCCCGCTGG 480

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Db 61 CCACCCCTCCGAGCCTTACCAGAACCCAGCCCTGCTCTCTCCCGCAAACTCGGTGG 120
QY 481 GTTGTCCCAACGCAACAGAAACCGCGCTTTGGGCAGAGCGGAGGGCTGGCAGCGATAGC 540
Db 121 GTTGTCCCAACGCAACCGCAACCTCGTATGTTGTTGAGGAGCGTGGACAGCAGTGGC 180
QY 541 AACTCTCTCGAAGCGTCCAGCCTTAATCTG-----CCCCCAGC 579
Db 181 TCCTCGAGTGGTGGAGGGTCCGCAATGGAGCGGAGGTGGCCACCAGGGCTCCGGCGCC 240
QY 580 GTCCGAATCCCAACCCCGTCTCTGAAAACTGAAGGCTGTACAGCTACAAACCCGAAAGAG 639
Db 241 ATCGAGTCCCATCCCGCTCTTGAAGAAAGCTGTGCGGCACACAGCTACAAACCCGAGG 300
QY 640 TTTGAGTGAATCTGAAAGCGGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGAC 699
Db 301 TTCGATTGGAACCTGAAAAATGGCCGGGTGTTTCATCATTAAGAGCTACTCTGAGGACGAC 360
QY 700 ATCCACCGCTCCATTAAGTACTCCATCTGGTGTAGCAGACGCGGCACAGCGCCTG 759
Db 361 ATCCATCGCTCCATCAAGTACTCCATCTGGTGCAGCAGCGAAACATGGAACCAAGCGCTG 420
QY 760 GACAGCGCTTCCGCTGATGAGCAGCAAGGGGCGGCTACTCTCTTCAGCGTCAAT 819
Db 421 GATTCGCGTTTCGTGCCATCAACGGCAAGGTCTCTACTCTGTTTCAGCGTCAAC 480
QY 820 GCGAGTGGGCATTTTGTGGGTGGCGAGATGAAGTCCCGCTGGAGCTACGCGCCACTG 879
Db 481 GCGAGCGGACATCTCTGTGGCGTGGCGAGATGCGTTCGCTGTGACTACGCGCCACTG 540
QY 880 GCGGGGTCTGCTCTCAGACCAAGTGGAGGGGAATTTGATGTCCAGTGGATTTTGTGTT 939
Db 541 GCGCGTGTGTGGCGCAGGACCAAGTGGAGGGCAATATGATGTGGACTGGCTGTGTGTC 600
QY 940 AGGATGTACCAATAACAGCTCCGGCACATCAGGCTG 978
Db 601 AAAGACGTGCCCAACAGTCAGCTCAAGCGCATGCGCGCTG 639

RESULT 70
AW168034 740 bp mRNA linear EST 29-JAN-2001
LOCUS AW168034 Ol-br-ad cDNA Oryzias latipes cDNA clone br1650, mRNA
DEFINITION sequence.
ACCESSION AW168034
VERSION AW168034.1 GI:12590103
KEYWORDS EST.
SOURCE Japanese medaka.
ORGANISM Oryzias latipes
REFERENCE 1 (bases 1 to 740)
AUTHORS Mita, K., Ishikawa, Y. and Yamauchi, M.
TITLE Establishment of cDNA database of medaka, Oryzias latipes
JOURNAL Unpublished (2001)
COMMENT Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmिता@nirs.go.jp
method:uni-directional sequence direction:sequenced from T3 primer
(5' -> 3').
Location/Qualifiers
1. .740
/organism="Oryzias latipes"
/strains="HNI"
/db_xref="taxon:8090"
/clone_lib="br1650"
/sex="female/male mixed"
FEATURES
source

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/tissue_type="brain"
/dev_stage="adult"
BASE COUNT 196 a 204 c 167 g 173 t
ORIGIN

Query Match 13.4% Score 271.4; DB 1; Length 740;
Best Local Similarity 78.2; Pred. No. 1.9e-58;
Matches 326; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 1 CAAAGGACAGAGATAAATAAGTCAAAATGGTTCGTTACATCAGAAGGATACAGTTCATG 60
Db 315 CAAAGGACAGAGATCTAAAGTCAAAATGGTTCGTTACATCAGAAGGATCTGTCATG 374

Qy 61 ACAATGACTTTGAGCCCTACCTTACTGGACAGTCAAAATCAGAGTAACAGTTACCCCTCAA 120
Db 375 ATAATGACTTTGAGCCATACCTTACCAGTCAGTCAAGCAGATAAAGAGTACCAGTCCA 434

Qy 121 TGAGGACCCCTACTCTCCAGCTATTACCCGCGTCCATTTGGATTTCCTTACTCCCTCA 180
Db 435 TCATGATCCTTACTCTCCAGCTACTATGCTCTCTTATTGGATTTCCTGTTCCGTTACCCTAA 494

Qy 181 ATGAGGCTCCGTGCTACTCTCAGGGAGCCCTCCGATTCCATCTCACCACTACCGAC 240
Db 495 GTGAGGCTCCGTGCTACTCTGTTGGGATCCACTATTTCATACCTCACACCTATGGAC 554

Qy 241 AGCTCAGTAACGAGACATCATTTTATGACAGATGCTGTTTTTGGGAGCGCTGGGGGCC 300
Db 555 CTTTGGAGCAATGGAGACCATCATCTCATGCGGACACCGTGTGTTGGGAGCGCGAGGGGTC 614

Qy 301 TGGGGACACATCATCATCAGACAGGTTCAATTTTTTCCCTGAAAACCCCTGCTTCTCAG 360
Db 615 TGGGAAGCAGCATCTACCGGACAGGTTTAACTTTTTTCCCTGAAAACCCCGCTTCTCTG 674

Qy 361 CATGGGGACAAAGTGGGTCTCAAGTCAGACAGCCAGAGCTCAGCCTCTCCCGACA 417
Db 675 CTTGGGGAACAGTGGCTCCAGGGTCAGCAGACTCAAAATTCGCGCTATGGTGCCA 731

RESULT 71
AA928886 391 bp mRNA linear EST 07-JUL-1998
LOCUS
DEFINITION
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 391)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 514 Std Error: 0.00
Seq primer: -40mb fwd. ET from Amersham
High quality sequence stop: 322.
Location/Qualifiers
1..391
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1568259"
FEATURES
source

/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; let strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 89 a 64 c 96 g 142 t
ORIGIN

Query Match 13.4% Score 271; DB 1; Length 391;
Best Local Similarity 100.0%; Pred. No. 2.1e-58;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1758 GAAATCTTTCCTTCAGATCTGTGCCCACTGAACAGCCACCGTCCCTCAGTCTCCTG 1817
Db 1 GAAATCTTTCCTTCAGATCTGTGCCCACTGAACAGCCACCGTCCCTCAGTCTCCTG 60

Qy 1818 GTGTCCGATTTGGGCTGGATGTTGGGCGATGATGTGGAGAACTGGAAGTGTCTT 1877
Db 61 GTGTCCGATTTGGGCTGGATGTTGGGCGATGATGTGGAGAACTGGAAGTGTCTT 120

Qy 1878 AGTCTCTGTTTCAGGCTCGGCGATCTTTGTTGTTGTCACATCTTTTAAATTTTACACCT 1937
Db 121 AGTCTCTGTTTCAGGCTCGGCGATCTTTGTTGTTGTCACATCTTTTAAATTTTACACCT 180

Qy 1938 TTTCTTAAGAAATCTTAATGCGCTTAAGTTTATTTTATACCAATTAATGCTGAGCTTAAAGT 1997
Db 181 TTTCTTAAGAAATCTTAATGCGCTTAAGTTTATTTTATACCAATTAATGCTGAGCTTAAAGT 240

Qy 1998 TAGATCTGTTACTACAGACAGTGTGATGCA 2028
Db 241 TAGATCTGTTACTACAGACAGTGTGATGCA 271

RESULT 72
AA116778/c
LOCUS
DEFINITION
2601658 3' similar to TR:064526 064526 YUPB8H12R.13 PROTEIN. ; mRNA
sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AA116778.1 GI:6083116
EST.
zebrafish.
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 391)
Sugano, S., Kawakami, K., Johnson, S., Li, F., Marra, M., Bddy, S.,
Hillier, L., Clifton, S., Allen, M., Gibbons, M., Jost, S., Kucaba, T.,
Martin, J., Pape, D., Steptoe, M., Underwood, K., Theising, B., Ritter
, E., Bowers, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU Zebrafish EST Project 1999
Unpublished (1999)
Contact: S.L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
Sequencing by: Washington University Genome Sequencing Center
Seq primer: T7 ET from Amersham
High quality sequence stop: 308.
Location/Qualifiers
1..391
/organism="Danio rerio"
FEATURES
source
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/clone="2601658"
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/sex="mixed (one male and one female, including unfertilized eggs)"
/dev_stages="adult"
/lab_host="DH10B (phage resistant)"
/note="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTTCCTCTCTAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA. " 93 t
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BASE COUNT 80 a 115 c 103 g 93 t

ORIGIN

Query Match 13.3%; Score 270.6; DB 2; Length 391;  
Best Local Similarity 81.0%; Pred. No. 2.6e-58;  
Matches 315; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 661 GGGCGTGTTCATCATCAGAGCTACTCTGAGGAGCAGATCCACCGCTCCATTAGTAC 720  
DB 390 GGGCGGTGTTCATCATTAAGAGCTACTCTGAGGAGCAGATCCATCGCTCCATCAAGTAC 331  
QY 721 TCCATCTGGTGTAGCAGACGCGCAACAGCGCTGTGAGCAGCGCTTCCGCTGCATC 780  
DB 330 TCCATCTGGTGTAGCAGCGAGACATGAGACAGCGCTGTGATCTCGGTTCTGCGCATC 271  
QY 781 AGCAGCAAGGGGCGGCTTACTCTCTTTCAGCGTCAATGGGAGTGGGCATTTTGTGGG 840  
DB 270 AACGGCAAGGTCTGTCTACTCTGTCTCAGCGTCAACGCGCAGCGACACTTCTGTGGC 211  
QY 841 GTGGCCGAGATGAAGTCCCGGTGGACTAGCGCAGGTCGCGGGTCTGGTCTCAGGAC 900  
DB 210 GTGGCGGAGATGCGTTCGCGCTGTGTGACTAGCGCAGGTCGCGGTGTGGGCGCAGGAC 151  
QY 901 AAGTGAAGGGGAAGTTTGATGTCCAGTGATTTTGTGAAGATGTACCCATAACCCAG 960  
DB 150 AAGTGAAGGGCAATTTGATGTGGACTGTCTTGTGTAAGACGTGCGCCACACATCAG 91  
QY 961 CTCGGGCATCAGGTGGAGATAACGACACAAACCGGTCTCAAACTCCCGGACACC 1020  
DB 90 CTCAGGCACATCCGCTGGAGACATGACACAGCCCGTGACCAACTCGCGTGACACA 31  
QY 1021 CAGGAGTGCCTTAGAAAAAGCCAAAGCA 1049  
DB 30 CAGGAGTGCCTCTGGAAGAGGCCAAAGCA 2

RESULT 73

AW116788/c  
LOCUS AW116788.1 387 bp mRNA linear EST 20-OCT-1999  
DEFINITION f19h06.x1 Sugano Kawakami zebrafish DNA Danio rerio cDNA clone 2601659 3', similar to TR:064526 O64526 YUP8H12R.13 PROTEIN. ;, mRNA sequence.

ACCESSION AW116788  
VERSION AW116788.1 GI:6083126  
KEYWORDS zebrafish.  
SOURCE Danio rerio.  
ORGANISM zebrafish.

REFERENCE 1 (bases 1 to 387)  
AUTHORS Sugano,S., Kawakami,K., Johnson,S., Li,F., Marra,M., Eddy,S.,

Hillier,L., Clifton,S., Allen,M., Gibbons,M., Jost,S., Kucaba,T., Martin,J., Pape,D., Steptoe,M., Underwood,K., Theising,B., Ritter,E., Bowers,Y., Wylie,T., Waterston,R. and Wilson,R.  
WashU Zebrafish EST Project 1999  
Unpublished (1999)  
Contact: S.L. Johnson  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by: Washington University Genome Sequencing Center  
Seq primer: T7 ET from Amersham  
High quality sequence stop: 307.

FEATURES  
source 1..387  
/organism="Danio rerio"  
/strain="AB"  
/db\_xref="taxon:7955"  
/clone="2601658"  
/clone\_lib="Sugano Kawakami zebrafish DNA"  
/sex="mixed (one male and one female, including unfertilized eggs)"  
/dev\_stages="adult"  
/lab\_host="DH10B (phage resistant)"  
/note="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTTCCTCTCTAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA. " 93 t

BASE COUNT 79 a 113 c 102 g 93 t

ORIGIN

Query Match 13.3%; Score 269.2; DB 2; Length 387;  
Best Local Similarity 81.1%; Pred. No. 5.9e-58;  
Matches 313; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 664 CGTGTGTTCATCATCAGAGCTACTCTGAGGAGCAGATCCACCGCTCCATTAGTACTCC 723  
DB 387 CGGGTGTTCATCATTAAGAGCTACTCTGAGGAGCAGATCCATCGCTCCATCAAGTACTCC 328  
QY 724 ATCTGTGTAGCAGACGCGCAACAGCGCTGTGAGCAGCGCTTCCGCTGCATGAGC 783  
DB 327 ATCTGTGTAGCAGCGGAACATGGAACACAGCGCTGGATTCTGCGTTTCTGCCATCAAC 268  
QY 784 AGCAAGGGGCGGCTTACCTCTTTCAGCGTCAATGGGAGTGGGCATTTTGTGGGGTG 843  
DB 267 GGCAGAGGTCTGTCTACCTGTCTCAGCGTCAACGCGCAGCGACACTTCTGTGCGGTG 208  
QY 844 GCGGAGATGAAGTCCCGGTGACTACGCGCAGTGC CGGGGTCTGGTCTCAGGACAG 903  
DB 207 GCGGAGATGCGTTCGCGCTTGTACTACGCGCAGTGC CGGGGTGTTTGGGCGCAGGACAAG 148  
QY 904 TCGAGGGGAAGTTTTCATCTCCAGTGGATTTTTTGTAAAGGATGTACCCAATACCAAGCTC 963  
DB 147 TGAAGGGCAAAATTTGATGTGAGCTGGCTGTTTGTAAAGAGCTGCGCCCAACAGTCAAGCTC 88  
QY 964 CGGCACATCAGCGCTGGAGAAATAACGACAAACAAACCGGTTCACAAACTCCCGGGACACCCAG 1023  
DB 87 AGGCACATCCGCTGGAGAAACATGACAAACAGCCCGTGCACCAACTCCGCGTGACACACAG 28  
QY 1024 GAGGTGCCCTTAGAAAAAGCCAAAGCA 1049  
DB 27 GAGGTGCCCTCTGGAAGAGGCCAAAGCA 2

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RESULT 74
AA633904/c
LOCUS
DEFINITION
ac73a10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:868218 3' similar to TR:G849195 G849195 CHROMOSOME IV COSMID
9481. ; mRNA sequence.
ACCESSION
AA633904
VERSION
AA633904.1 GI:2557118
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 652)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
J., Moore, B., Scheinberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R., and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Insert Length: 1199 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 470.
FEATURES
source
1. .652
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:868218"
/clone_lib="Stratagene lung (#937210)"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/notes="Organ: lung; Vector: pBluescript SK-; Site 1: EcoRI
; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
dT, normal lung. Average insert size: 1.0 kb; Uni-ZAP XR
Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3'
adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3'"
BASE COUNT 164 a 155 c 130 g 203 t
ORIGIN
Query Match 13.2% Score 266.8; DB 1; Length 652;
Best Local Similarity 74.1%; Pred. No. 2.8e-57;
Matches 351; Conservative 0; Mismatches 122; Indels 1; Gaps 1;
Qy 700 ATCCACCGCTCCATTAAAGTACTCCATCTGGTGTAGCAGACGCGCAACAGCGCTG 759
Db 652 ATCCACCGTTCATTAGTATAATTTGGTGCAGCAGCAGCATGTTACAGAGACTG 593
Qy 760 GACAGCGCTTCCCGCTGTAGCAGCAAGGGGCCGCTTACCTGCTCTTCAGCGTCAAT 819
Db 592 GATGCTGCTTATCGTTCATGAACGGGAAGGCCCGCTTACTTACTTTTCAGTGTCAAC 533
Qy 820 GGGAGTGGGCAATTTTGTGGGGTGGCGAGATGAAGTCCCGTGGACTACGGCACCAGT 879
Db 532 GCGAGTGGACACTTCTGTGGCGTGGCAGAAATGAATCTGCTGGGACTACACACATGT 473
Qy 880 GCCGGGCTCTGGTCTCAGGCAAGTGAAGGGGAAGTTTGAATCTCCAGTGGATTTTGT 939
Db 472 GCAGGTGTGGTCCCGAGCAATGGAAGGGTCTGTTGATGTGAGTGGATTTTGTG 413
Qy 940 AAGGATGTACCAATACCCAGCTCCGGCAGCATACGGCTGGGAATACGACAAACCG 999

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Db 412 AAGGAGCTTCCCAATAGCCAACTGCGACACATTCGGCTAGAGAACACCGAGATTACCCA 353
Qy 1000 GTCAAACTCCCGGACACCCAGAGAGTGCCTTTAGAAAAAGCCAGCAAGTCTGTA 1059
Db 352 GTGACCACTCTAGGACACTCAGAGAGTGCCTCTCGAAAAAGCTAAGCAGGTGTTGAAA 293
Qy 1060 ATTATCAGTTCCTTACAGACACAACTCTCATCTTCGACGACTTTTGTCTACTAGGAGAAG 1119
Db 292 ATTATAGCCAGCTTACAAGCACACCACTTCCATTTTGTGACTTCTCACAATATGAGAAA 233
Qy 1120 CGCC-AGAGGAGGAGGAGTGGTGGCGAAGGACGCGAGAGTCCGAAACAAACA 1172
Db 232 CGCCAGAGGAGAGAAAGAGTGTAAAGGAAGACGTCAAGGTCTGGGAAATAA 179

RESULT 75
AA637425
LOCUS
DEFINITION
YU06d08.r1 Soares mammary_gland NDMMG Mus musculus cDNA clone
IMAGE:1179855 5' similar to TR:G849195 G849195 CHROMOSOME IV COSMID
9481. ; mRNA sequence.
ACCESSION
AA637425
VERSION
AA637425.1 GI:2561013
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 476)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Scheinberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:637703
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 467.
FEATURES
source
1. .476
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1179855"
/clone_lib="Soares_mammary_gland_NDMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notes="Organ: mammary gland; Vector: p773D-Pac (Pharmacia
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTTACCAATCTGAAGTGGGAGCGCGGATGTTTCTTTTCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified p773 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonafido."
BASE COUNT 148 a 98 c 121 g 108 t 1 others
ORIGIN

```

```
Query Match 13.1%; Score 265.2; DB 1; Length 476;
Best Local Similarity 73.7%; Pred. No. 6.5e-57;
Matches 350; Conservative 0; Mismatches 124; Indels 1; Gaps 1;

QY 703 CACCGCTCCATTAACTCCATCTGGTGTAGCAGACAGCGGCAACAGCGCTGGAC 762
Db 1 CACCGTTCATTAAATATATCTGGTGCAGCAGACATGGTAAAGAGACTGGAT 60

QY 763 AGCGCTTCCGCTGCATGACGAGCGGCGCGCTTACTCTCTTCAAGCTCAATGG 822
Db 61 GCGGCTTATCGTTCATGAATGGAAGGGTCCCGTGTACTTACTTTCAGTGTCAACG 120

QY 823 AGTGGGCAATTTTGGGGTGGCCGAGATGAAGTCCCGTGGACTACGCGACAGTGCC 882
Db 121 AGTGACACATCTGTGGAGTTCGAGAGATGAATCTGCTGTGGACTACACACATGTG 180

QY 883 GGGGTCTGTCTCAGACAAAGTGAAGGGAGTTTGATGTCCAGTGAATTTTGTAA 942
Db 181 GGTGTGTGTGCCAGACAAATGGAAGGGTCTGTCGATGTGAGATGGATTTTGTGA 240

QY 943 GATGTACCAATAACAGCTCCGCGCACATCAGGCTGGAGATTAACGACAAACCGGTC 1002
Db 241 GAGTTCCTCCATAGCACTCGCACATCTGCTAGAGAACACGAGATTAACAGTG 300

QY 1003 ACAACTCCCGGACACCCAGAGGTGCGCTTAGAAAAAGCAAGAGTGTGAAATP 1062
Db 301 ACCAACTCTAGNGATCTCAGGAAGTGCCTCTGGAAGAGCTAAGCAGGTGTGAAATC 360

QY 1063 ATCAGTCTTACAGCACACACCTCCATCTTCGAGCACTTTGCTCAGTACGAGAGCG 1122
Db 361 ATAGCCAGCTAGAACACACCACTTCCATTTTGTGATCTTCTCACACTATGAGAAAGC 420

QY 1123 C-AGAGGAGGAGGTGTGGCGCAAGGAGGAGCGAGTGGAAACAAACAAATGAG 1176
Db 421 CAAGAGGAGAGAAAGTGTAAAGAGGAGCTCAAGTGTGGGAAATAGAAAG 475

RESULT 76
AA711690
LOCUS 594 bp mRNA linear EST 24-DEC-1997
DEFINITION v058b06.kl Soares mammary_gland NbMWG Mus musculus cDNA clone
IMAGE:1195571 5' similar to TR:04503 004503 SEQUENCE OF BAC F21M12
FROM ARABIDOPSIS THALIANA CHROMOSOME 1, COMPLETE SEQUENCE. ;, mRNA
sequence.
ACCESSION AA711690.1 GI:2721608
VERSION AA711690
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 594)
Giesel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LILNL; contact the
IMAGE Consortium (info@image.lilnl.gov) for further information.
MGI:642667
Possible reversed clone: similarity on wrong strand
Seq primer: -28m3 rev2 ET from Amersham
High quality sequence stop: 501.
Location/Qualifiers

1. 594
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/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notes="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
RI; lsc strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTTACCAATCTGAAGTGGGAGCGCGCGCAATGTTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
BASE COUNT 153 a 168 c 150 g 123 t
ORIGIN

Query Match 13.0%; Score 263.6; DB 1; Length 594;
Best Local Similarity 83.8%; Pred. No. 1.8e-56;
Matches 310; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

QY 399 AGCTCAGGCTCTCCAGCAGACGCGCGCTGGCTCAACCGCAGTATCAGAGCCCTCA 458
Db 224 AGCTCAACCTCTCTCTGTTCCAGCCCCCACCCTTGTCCAGCCACAGTATCAGAGCCCTCA 283

QY 459 GCAGCCACCCAGACGCGCTGGGT-TGCCCCACGCAACAGAAACGCGGCTTTGGGCAGA 517
Db 284 GCAGCCACTTCAACCCCGCTGGTGGGCTCTCGAAACAGAAATCGAGCATTTGGGCAGA 343

QY 518 GCGGAGGGGCTGGCGGATGACAACTCTCTCTGGAAAGCTCCAGGCTTAATTTGCCCCCA 577
Db 344 GTGGAGGGGCGCAACAGTACAGTAACTCTGTGGAAATGCCCAACCTACTTCTGCCCGCA 403

QY 578 GCGTGAATCCACCCCGCTCTTGAAGAACTGAAGGCTGCTCAGAGCTACACCCGAAAG 637
Db 404 GTGTGAATGCCACCCCTGTCTGGAGAACTGAAGAGCTGCCACAGCTATAACCCCTAAAG 463

QY 638 AGTTTGAAGTGAATCTGAAAGCGGCGTGTCTTCATCATCAAGAGCTACTCTGAGGAG 697
Db 464 AGTTGAGCTGGAATCTTAAGAGTGGCGGGTGTTCATCATCGAGGACTTCTGAGGAG 523

QY 698 ACATCCACCGCTCCATTAAAGTACTCCATCTCTGTGTAGCAGACGCGCAACAGCGCC 757
Db 524 ACATCCACCGCTCCATCAAGTACTCCATCTGTGTAGTGTAGTGAACAGGCAACAGCGCC 583

QY 758 TGGACAGCGC 767
Db 584 TGGACAGCGC 593

RESULT 77
AA121411
LOCUS 527 bp mRNA linear EST 19-NOV-1996
DEFINITION zn78e03.kl Stratagene NT2 neuronal precursor 937230 Homo sapiens
cDNA clone IMAGE:564316 5', mRNA sequence.
ACCESSION AA121411
VERSION AA121411.1 GI:1679234
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 527)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chlasse,S., Dietrich,N., Dubuque,T., Favellio,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le.N., Mardis,E., Moore
```

B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 5 (9), 807-828 (1996)

97044478  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: setowatson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 415.

#### FEATURES

source  
1. .527  
/organism="Homo sapiens"  
/db\_xref="GDB:4596839"  
/db\_xref="taxon:9606"  
/clone="IMAG:564316"  
/clone\_lib="Stratagene NT2 neuronal precursor 937230"  
/tissue\_type="neuroepithelial cells"  
/dev\_stage="Ntera-2 neuroepithelial cells"  
/lab\_host="SOLR (kanamycin resistant)"  
/notes="Organ: brain; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Uninduced, exponentially growing neuroepithelial cells (Ntera-2/ci.D1). Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCAGG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' 88 t 4 others  
BASE COUNT 123 a 175 c 137 g 88 t 4 others  
ORIGIN

Query Match 12.9%; Score 262; DB 1; Length 527;  
Best Local Similarity 90.8%; Pred. No. 4.4e-56;  
Matches 334; Conservative 0; Mismatches 27; Indels 7; Gaps 5;  
QY 387 CAGCAGACCCAGAGCTCAGCTCTCCAGCAGACGCCCGCTTGGCTCAACCGCAGTA 446  
DB 133 CAGCCAGCAGGTGGCTCAGCTCTCCAGCAGACGCCCGCTTGGCTCAACCGCAGTA 191  
QY 447 TCAGAGCCCTCAGCAGCCAGCCCGCTGGGTGGCCCGCAGCAGAACGCGGC 506  
DB 192 TCAGAGCCCTCAGCAGCCAGCCCGCTGGGTGGCCCGCAGCAGAACGCGGC 251  
QY 507 GTTTGGCAGCGAGGGGTGGCAGCGATAGCAACTCTCC-TGGAAAGCTTCAGCCTA 565  
DB 252 GTTTGGCAGCGAGGGGTGGCAGCGATACAACTCTCTTTGGAAGCGTCCAGCCTA 311  
QY 566 ATTCTGCCCC-AGCGTCGAATCCACCCCGCTCC--TTGAAACTGAAGCTGCTCAC 621  
DB 312 ATTCTGCCCCAAGCGTCGAATCCACCCCGCTCTTTGAAACTGAAGCTGCTCAC 371  
QY 622 AGCTACAAACCCGAAAGAG-TTTGAGTGGAACTCTGAAAGGGGGGGGTGTTCATCATCAA 680  
DB 372 AGCTACAAACCCGAAAGAGTTTGGTGGAACTCTGAAAGGGGGGGGTGTTCATCATCAA 431  
QY 681 GAGTACTCTGAGAGCAGATCCACCGCTCCATTAGTACTCCCATCTGGTGTAGCAGAGA 740  
DB 432 GAGTACTCTGAGAGCAGATCCACCGCTCCATTAGTACTCCCATCTGGTGTAGCAGAGA 491  
QY 741 GCACGGCA 748  
DB 492 GCACGGAA 499

#### RESULT 78

BB645804  
LOCUS  
DEFINITION  
BB645804 695 bp. mRNA linear EST 26-OCT-2001  
BB645804 RIKEN full-length enriched, 10 days neonate medulla oblongata Mus musculus cDNA clone B830001A02 5', mRNA sequence.

#### ACCESSION VERSION KEYWORDS SOURCE ORGANISM

BB645804  
BB645804.1 GI:16480217  
EST.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 695)  
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, F., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
Unpublished (2001)

#### REFERENCE AUTHORS

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.  
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.  
e mouse tissues.

#### Location/Qualifiers

1. .595  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="B830001A02"  
/clone\_lib="RIKEN full-length enriched, 10 days neonate medulla oblongata"  
/tissue\_type="medulla oblongata"  
/dev\_stage="10 days neonate"  
/lab\_host="DH10B"  
/notes="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second

#### FEATURES source

**JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)**

Clone distribution: MGC clone distribution



found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
 Plate: L16M314 row: f column: 08  
 High quality sequence stop: 629.

## FEATURES

Location/Qualifiers  
 1. .629  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3628807"  
 /clone\_lib="NIH\_MGC\_19"  
 /tissue\_type="neuroblastoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: brain; Vector: pOT87; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
 Note: this is a NIH\_MGC Library."

BASE COUNT 203 a 122 c 152 g 152 t

Query Match 12.6%; Score 255.6; DB 2; Length 629;  
 Best Local Similarity 74.4%; Pred. No. 1.9e-54; Indels 1; Gaps 1;  
 Matches 335; Conservative 0; Mismatches 114;

QY 724 ATCTGGTGTAGCACAGACGCGCAACAGCGCCCTGGACAGCGCTTCCGCTGCATGAGC 783  
 Db 7 ATTTGGTGCACACAGACAGCTGTTAAACAAGAGACTGGATGCTGTATCGTTCCATGAAC 66  
 QY 784 AGCAAGGGGCGCTTACCTGCTCTTACGCTCAATGGAGTGGGCATTTTGTGGGGTG 843  
 Db 67 GGGAAAGGCGCCGTTACTTACTTTTCACTGTCAACGCGCAGTGGACACTTCTGTGGCGTG 126  
 QY 844 GCCGAGATGAATCCCGCTGGACTACGGCACCAGTGCAGCGGCTGTCTCAGGACAAAG 903  
 Db 127 GCAGAAATGAATCTGCTGTGGACTACACACATGTGCAGGTGTGTGCTCCAGGACAAA 186  
 QY 904 TGGAAAGGGGAAGTTTGATGTCCAGTGGATTTTGTGTAAGGATGTACCCAAATACCAAGCTC 963  
 Db 187 TGGAAAGGTGCTTTTGATGTCCAGTGGATTTTGTGAGGAGCTTCCCAATAGCCAAGT 246  
 QY 964 CGGCACATCAGCTGGAGATTAACGACAAACAAACGGTGCACAACTCCCGGAGACCCAG 1023  
 Db 247 CGACACATTCCTCTAGAGAAACAGGAAATAAACAGTGCACCACTCTAGGCGACACTCAG 306  
 QY 1024 GAGTGCCTTTAGAAAAGCAAGCAAGTGTGAAATTTATCAGTTCTTACAAGCACACA 1083  
 Db 307 GAAGTGCTCTGGAAGAGCTTAAGCAGTGTGTAATTTATAGCCAGCTACAAGCACACC 366  
 QY 1084 ACCTCCATCTTCGACGACTTTTGTCTCACTACGAGAACGCC-AGAGGAGGAGGAGGTGTG 1142  
 Db 367 ACTTCCATTTTGTGATCTTCTACACTATGAGAAACGCCAAGAGGAGGAGAAAGTGT 426  
 QY 1143 CGAAGGAACGGCAGAGTCGAAACAAACAA 1172  
 Db 427 AAAAAGGAACGTCAGGTCTGTTGGGAAATAA 456

RESULT 81  
 AL680804 AL680804 XGC-gastrula Silurana tropicalis cDNA clone TGas070b10 5',  
 LOCUS mRNA sequence.  
 DEFINITION

AL680804 AL680804.1 GI:19537178  
 VERSION EST.  
 KEYWORDS western clawed frog.  
 SOURCE Silurana tropicalis  
 ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 Xenopodinae; Silurana.  
 REFERENCE 1 (bases 1 to 623)

## AUTHORS

Taylor, R., Ashurst, J.L., Croning, M.D.R., Zorn, A.M. and Rogers, J.  
 Sanger Xenopus tropicalis EST project 2002  
 Unpublished (2001)  
 JOURNAL  
 COMMENT

Contact: Taylor R  
 Sanger Centre  
 Hinxton, Cambridgeshire, CB10 1SA, UK  
 Email: trop@sanger.ac.uk  
 Sanger Xenopus tropicalis EST project 2001  
 TROPICALIS\_SEQUENCE ID: TGas070b10.p1cSP6  
 Sequencing primer: p1cSP6  
 This sequence is from a Xenopus Gene Collection (XGC) library  
 constructed by Aaron M. Zorn.

## FEATURES

Location/Qualifiers  
 1. .623  
 /organism="Silurana tropicalis"  
 /db\_xref="taxon:8364"  
 /clone="TGas070b10"  
 /clone\_lib="XGC-gastrula"  
 /dev\_host="gastrula (stages 10.5-13 mixed)"  
 /lab\_host="Escherichia coli XL1-blue"  
 /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from 5' of poly A+ RNA from stages 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

BASE COUNT 184 a 133 c 153 g 153 t

Query Match 12.2%; Score 246.8; DB 1; Length 623;  
 Best Local Similarity 73.0%; Pred. No. 3.4e-52;  
 Matches 317; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 691 GAGGACGACATCCACCGCTCCATTAAAGTACTCTCCATCTGGTGTAGCAGACGACGCGCAAC 750  
 Db 12 GAGATGACATTCACCGCTCCATCAGTACATGTTTGGTGTCTACAGACATGGTAAAC 71  
 QY 751 AAGCGCTGGACAGCGCTTCGCTGCATGAGCAGCAAGGGGCGCGTCTACCTGCTCTTC 810  
 Db 72 AAGCGCTGGATGCAGCTTATCGCTCTCTTAATGGCAAGGTCACATTTACCTGCTTTT 131  
 QY 811 AGCGTCAATGGGAGTGGGCATTTTGTGGGTGGCCAGATGAAGTCCCGTGGACTAC 870  
 Db 132 AGTGTAAATGGTAGTGGCCACTTCTGTGGAGTTGACAGAAATGGCGCTCAGCAGTAGACTAT 191  
 QY 871 GGCAACAGTCCCGGGTCTGCTCTCAGGACAAAGTGGAGGGGAAGTTTGTGTCAGTGG 930  
 Db 192 AATACTTGTGGGAGTTTGGTACAGGACAAATGGAGGGCGCTTGTGTCGGCTGG 251  
 QY 931 ATTTTGTTAAGGATGTACCCAAATACAGCTCCGGCACATCAGGCTGGAGAAATACGAC 990  
 Db 252 CTTTTTGTCAAGGATGTACCTAATGGACAGTTACGTCACTTCGTCTAGAGAACATGAC 311  
 QY 991 AACAAACGGTCAAACTCCGGGACACCCAGGAGGTGCCCTTAGAANAAGCCAGCAA 1050  
 Db 312 AACAAACGAGTCACCAACTCTCCGGGACACCAAGAGGTGCCATTGGAAAGAGCCGACAG 371  
 QY 1051 GTGCTGAAAATTTACAGTTCTCTACAAGCACACACCTCCATCTTCGACGACTTTGTCTCAC 1110  
 Db 372 GTGCTTCGATTCATTTGCCAGCTACAGCACACACCTCCATCTTTGATGATTTTCTCAT 431  
 QY 1111 TACGAGNAGCGCCA 1124  
 Db 432 TATGAGAAGAGGCA 445

## RESULT 82

AW510247/c

LOCUS

DEFINITION

AW510247

similar to TR:064526 O64526 YU98H12R.13 PROTEIN. ;contains Alu

repetitive element;; mRNA sequence.

ACCESSION

AW510247

VERSION

AW510247.1 GI:7148325

675 bp mRNA linear EST 03-MAR-2000  
 fkl1c02.x1 zebrafish fin day3 regeneration Danio rerio cDNA 3'



**KEYWORDS** EST.  
**SOURCE** zebrafish.  
**ORGANISM** Danio rerio.  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
**AUTHORS** Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.  
**TITLE** WashU Zebrafish EST Project 1998  
**JOURNAL** Unpublished (1998)  
**COMMENT** Contact: Stephen L. Johnson  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: zbrafish@watson.wustl.edu  
 cDNA Library Preparation: Raymond Lee. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center. Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and ResourceCenter@primaridatenbank, Berlin, Germany (web address: www.rzpd.de)  
 Seq primer: T7 ET from Amersham  
 High quality sequence stop: 218.  
**FEATURES** Location/Qualifiers  
 source  
 1..675  
 /organism="Danio rerio"  
 /db\_xref="taxon:7955"  
 /clone\_lib="zebrafish fin day3 regeneration"  
 /sex="mixed male and female"  
 /tissue\_type="3 day fin regenerates"  
 /lab\_host="E. coli XL0LR"  
 /note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; 1st strand cDNA primed with (GA)10ACTAGTCTCGAG(T)18, followed by second strand synthesis, and ligated to 5' adapter (5'-aatcgcgcagcag-3', 3'-gccgtgtc-5'. cDNA was cloned directionally (EcoRI/XhoI) into Stratagene Zap express lambda phage arms. Mass invivo excision done to obtain inserts in pBK-CMV phagenid."  
 BASE COUNT 162 a 170 c 164 g 179 t  
**ORIGIN**  
 Query Match 12.1%; Score 245; DB 2; Length 675;  
 Best Local Similarity 71.8%; Pred. No. 9.9e-52;  
 Matches 348; Conservative 0; Mismatches 135; Indels 2; Gaps 2;  
 Qy 667 GTGTTTCATCATCAAGAGCTACTCTGTAGGACGACATCCACCGCTCCATTAGTACTCCATC 726  
 Db 675 GTCTACTTCTCCAAAGAGTACTCTATGGCGCATATCCACCGATCCATTACGGACTATATT 616  
 Qy 727 TGGTGTAGCACAGACGCGACACAGCGCTCGGACAGCGCTTCGCTGCATGACGACGC 786  
 Db 615 TGGTGCAGCGCAGCTCATGTCTCATAGCGGTGGACCCCTGTCATTCGGTTCGTAGCAAC 556  
 Qy 787 AAGGGCCCGCTC-TACTGCTCTTCACGCTCAATGGAGTGGGCATTTTGTGGGGTGGC 845  
 Db 555 ATAGGGCCACTCGTACTGCTGTTCAGTGTGATGATGCGATGGCCACTTCTGTGGCGTGGC 496  
 Qy 846 CGAGATGAAGTCCCCCGTGAATCAGGACACAGTCCGGGGTCTGTCTCAGGACAAGTG 905  
 Db 495 GTAGATGCGCTGCGCTGTGGCCCTTCAACACTTGTGAGGCGGTGTGGTCGAGGACAAGTG 436  
 Qy 906 GAAGGGGAAGTTGATGTCAGTGGATTTTGTGTAGGATGTACCAATAACAGCTCCG 965  
 Db 435 GAAGGGTGTGTTTGTATGTGGCGTGGATCTTTGTCAAGGACGTTTCCCAACAGCCCACTAAG 376

Qy 966 GCACATAGGCTGGGATATACGACAAACACCGGTCAAACTCCCGGACACCAGGA 1025  
 Db 375 GCACATTCGCTTGGAGAAACAATGAGATTAACCGGTAAACAACTCTCGACACACAGGA 316  
 Qy 1026 GTGCGCCCTTAGAAAAAGCAAGCAAGTCTGAAATATTCAGTTCCTCAAGCACACAAAC 1085  
 Db 315 GGTTCCTCTAGACAAGGACGCTCAAGTGTGAGATCATCGGAGTTACAGCACACAC 256  
 Qy 1086 CTCATCTTCGACGACTTTTGTCTACTAGGAGAGCGCCA-GAGGAGGAGGAGGTGGTGG 1144  
 Db 255 CTCATCTTTGACGACTTCTCACACTACGAGAAACGTCAGGAGAGGAGGAGGAGTGTAAA 196  
 Qy 1145 CAGG 1149  
 Db 195 AAGG 191  
**RESULT** 83  
**LOCUS** AM149010 611 bp mRNA linear EST 03-NOV-1999  
**DEFINITION** xf08d09.x1 NCI CGAP Kid8 Homo sapiens cDNA clone IMAGE:2617457 3' similar to TR:O64526 O64526 YUP8H12R.13 PROTEIN. ; mRNA sequence.  
**ACCESSION** AM149010  
**VERSION** AM149010.1 GI:6196906  
**KEYWORDS** EST.  
**SOURCE** human.  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 611)  
**AUTHORS** NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
 Possible reversed clone: polyt not found  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 409.  
**FEATURES** Location/Qualifiers  
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 1..611  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2617457"  
 /clone\_lib="NCI CGAP Kid8"  
 /tissue\_type="renal cell tumor"  
 /lab\_host="DH10B"  
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.2 kb. Life technologies catalog #:  
 11524-014"  
 BASE COUNT 145 a 145 c 115 g 206 t  
**ORIGIN**  
 Query Match 12.1%; Score 244.4; DB 2; Length 611;  
 Best Local Similarity 73.7%; Pred. No. 1.4e-51;  
 Matches 311; Conservative 0; Mismatches 111; Indels 0; Gaps 0;  
 Qy 751 AAGCGCTCGACAGCGCTTCGCTGCATGACGACAAAGGCGCGCTTACCTGCTCTTC 810  
 Db 611 AGAGACTGGATGCTGCTTATCGTCCATGAACGGGAAGGCCCGCTTACTTCTTC 552  
 Qy 811 AGCGTCAATGGAGTGGGCATTTTGTGGGGTGGCGAGATGAAGTCCCGCTGGACTAC 870

Db 551 AGTGCAACGGCAGTGGACACTCTGTGGCGTGGCAGAAAATGAATCTGTGTGGACTAC 492

QY 871 GGCAACAGTGGCCGGGTCTGTGCTCAGGACAAAGTGGAAAGGGAAGTTGATGTCCAGTGG 930

Db 491 AACACATGTGAGGTGTGTGTCCAGGACAAATGGAAAGGTGCTTTGATGTCCAGTGG 432

QY 931 ATTTTGTGAAGTGTACCAATTAACCAAGCTCCGGCAGCATCAGGCTGGGAGAATAACGAC 990

Db 431 ATTTTGTGAAGGAGCTTCCCAATAGCCAAGTGGCAGACATTCGCTAGAGAACACAG 372

QY 991 AACAAACGGGTCAACAACTCCGGGACACCCAGGAGTGGCCCTTAGAAAAAGCCAAAGCAA 1050

Db 371 AATAAACAGGTGACCAACTCTAGGACACTCAGGAAGTGGCTCTGGAAAAAGGCTTAAGCAG 312

QY 1051 GTGCTGAAAATTTATCAGTTCTCAAGCACACAACTCCATCTTCGACGACTTTGCTCAC 1110

Db 311 GTGTTGAAAATTTATGACGAGTCAAGCACACCACTTCCTTTTGTGATGACTTCTCAC 252

QY 1111 TAGGAGAGCGCCAGGAGGAGGAGGTGTGCGCAAGGAACGGCAGAGTGGAAACAAAC 1170

Db 251 TATGAGAAACGCAAGAGGAAGAAAGTGTAAAGAAAGGAACGTCAGGTCTGTGGGAAT 192

QY 1171 AA 1172

Db 191 AA 190

RESULT 84

AW162686/c

LOCUS

DEFINITION

au87b11.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone

IMAGE:2783229 3' similar to TR:064526 O64526 YUP8H12R.13 PROTEIN.

! mRNA sequence.

AW162686

AW162686.1 GI:6301719

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 652)

Hillier,D., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Krizman,D., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin

J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,

White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU-NCI human EST Project

Unpublished (1997)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LML ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40UP from Gibco

High quality sequence stop: 469.

FEATURES

source

1. .652

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:2783229"

/organ\_lib="Schneider fetal brain 00004"

/sex="male"

/tissue\_type="frontal lobe"

/dev\_stage="5 months post-conception"

/lab\_host="DH108"

/notes="Organ: brain; Vector: pBluescript SK (Stratagene);

Site 1: SstI; Site 2: XhoI; Double-stranded cDNA was

prepared from human fetal brain tissue. 5' and 3'

adaptors were used in cloning as follows: 5' adaptor

sequence:

5'-GAGAGAGAGAGAGCTCAAGGATCTCTTAATTAATTAATCTCCCCCCCCCCC-3'

and 3' adaptor sequence:

5'-GAGAGAGAGACTCGAGTCTTTTTTTTTTTTTTTTTTT-3'. The library was

size-selected for >0.5 kb inserts and has an average

insert size estimated at 1.2 kb. This library was

constructed using the CAP-trapper method for full-length

enrichment and has not undergone amplification. Library

was constructed by Dr. Claudio Schneider (LNCIB-Area

Science Park, Trieste, Italy). "

BASE COUNT 153 a 158 c 123 g 218 t

ORIGIN

Query Match 11.9%; Score 241.2; DB 2; Length 652;

Best Local Similarity 72.9%; Pred. No. 9.1e-51;

Matches 337; Conservative 0; Mismatches 123; Indels 2; Gaps 2;

QY 713 TTAAGTACTCCATCTGTGTAGCACAGACGCGACACGCGCTGGACAGC-GCCTTC 771

Db 648 TAAAGTTAATAATTTGGCGAGGCACAGAGAGGGTAAACAAGAGACTGGGATGCTGTAT 589

QY 772 CGCTGCATGAGCAGAGGCGCCGCTACTCTCTTTCAGCGTCAATGGAGTGGGCAT 831

Db 588 CGTTCATGAACGGGAAGSCCGGTTTACTTTTAAGTGTCAACGCGAGTGGACAC 529

QY 832 TTTTGTGGGTGCGCGAGATGAAGTCCCCGTGGACTACGGCACCAGTCCGGGGTCTGG 891

Db 528 TTCTGTGGCGTGGCAGAAATGAAATCTGCTGTGGACTTACAACACATGTGCAGGTGTGTGG 469

QY 892 TCTCAGACAAAGTGGAGGGGAAGTTTGATGTCCAGTGGATTTTGTTAAGGATGTACCC 951

Db 468 TCCAGGACAAATGGAGGGTCTGTTTGTGATGTCCAGTGGATTTTGTGAAGGAGCTTCCC 409

QY 952 AATAACAGCTCCGGCAGCATCAGCTGGAGAAATAACGACAAACAAACCGGTCACAAACTCC 1011

Db 408 AATAGCCACTGGACACATTCGCTTAGAACAACGAGAAATAACGAGTGCACCACTCT 349

QY 1012 CGGACACCCAGAGTGGCCCTTAGAAAAAGCCAAAGCAAGTGTCTGAAAAATATCAGTTC 1071

Db 348 AGGACACTCAGGAAGTGCCTCTGGAAGGCTTAAGCAGGTGTGAAAAATTATAGCCAGC 289

QY 1072 TACAGCACACACCTCCATCTTCGAGGACTTTCCTACTACGAGAGGCC-AGAGGAG 1130

Db 288 TACAAGCACACCACTTCCATTTTGTGATGCTTCTCACCTATGAGAAACGCCAAGAGAA 229

QY 1131 GAGGAGTGTGGCGCAAGGACGCGAGAGTCGAAACAAACAA 1172

Db 228 GAAGAAAGTGTAAAAAGGAACGTCAGGTCTGTGGGAATAA 187

RESULT 85

AL675423

LOCUS

DEFINITION

AL675423 XGC-neurula Silurana tropicalis cDNA clone TNeu057m14 5',

637 bp mRNA linear EST 18-MAR-2002

AL675423

ACCESSION

AL675423.1 GI:19531797

VERSION

AL675423.1

KEYWORDS

EST.

SOURCE

western clawed frog.

ORGANISM

Silurana tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

Xenopodinae; Silurana.

1 (bases 1 to 637)

Taylor R., Ashurst, J. L., Croning, M. D. R., Zorn, A. M. and Rogers, J.

Sanger Xenopus tropicalis EST project 2002

Unpublished (2001)

Contact: Taylor R

Sanger Centre

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk

Sanger Xenopus tropicalis EST project 2001

TROPICALIS\_SEQUENCE\_ID: TNeu057m14.picSP6

Sequencing primer: PICSP6

This sequence is from a Xenopus Gene Collection (XGC) library

FEATURES  
source

constructed by Aaron M. Zorn.  
Location/Qualifiers  
1. .637  
/organism="Silurana tropicalis"  
/db\_xref="taxon:8164"  
/clone="TNeu057m14"  
/dev\_stage="neurala"  
/lab\_host="Escherichia coli DH10B"  
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA  
was oligo dt primed from Sug of poly A+ RNA from neurala.  
EcoRI-NotI cut cDNA was then ligated into pCS107 with  
EcoRI at the 5' end and NotI at the 3' end."  
BASE COUNT 129 a 235 c 149 g 123 t 1 others  
ORIGIN

Query Match 11.8%; Score 239.4; DB 1; Length 637;  
Best Local Similarity 78.7%; Pred. No. 2.6e-50;  
Matches 285; Conservative 0; Mismatches 77; Indels 0; Gaps 0;  
QY 1 CAAAGGACACAGATAAAGTACAAAGTTCGTTACATCAGAAAGGATACAGTTCATG 60  
DB 276 CAAACAATGATCTTATTCAGTTCAAAACGGATCCCTGCACCAAGGACAGCGTGCAG 335  
QY 61 ACAATGACTTTAGCCCTACTTACTGGACAGTCAATACAGATAACAGTTACCCCTCAA 120  
DB 336 ATAATGACTTCGAGCAGTACTCTCGGACAGTCCCAATCAGAGTAACAGCTACCCCTTCCA 395  
QY 121 TGAGCGACCCCTACCTGTCAGCTATTACCGCGGCTCCATTCGATTTCTTACTCCCTCA 180  
DB 396 TGACTGACCCGTCACCTGTCAGTTCATCCCTCTCTATCGGCTTTTCGGTATTCGCTCA 455  
QY 181 ATGAGGCTCGGTGCTTACTGACGGGACCCCTCCGATTCATATCCATCCCTACCGAC 240  
DB 456 GCGAAGCTCTTGCTCAACCGCGGGGACCCCGGATCCGTCACCTACCCCTACCGAC 515  
QY 241 AGCTAGTAAAGGACCATCAATTTATGACGATGCTGTTTTGGGACGCTGGGGGCC 300  
DB 516 AGCTAGCAACGGAGACCACTTTCATGACGATGCGGCTTTTGGGACGCGCGGGGCC 575  
QY 301 TGGGGAACACATCTATCAGCAGGTTCAATTTTCCCTGAAACCCCTGCGTTCTCAG 360  
DB 576 TNGGAATAACATCTATCAGCAGCGGTTCAATCTTCCCGGAAACCCCGGCTTTTCCG 635  
QY 361 CA 362  
DB 636 CA 637

RESULT 86  
AI561100/c

LOCUS 731 bp mRNA linear EST 13-MAY-1999  
DEFINITION tQ26c10.x1 NCI CGAP Utl1 Homo sapiens cDNA clone IMAGE:2209938 3'  
similar to TR:04503 004503 SEQUENCE OF BAC F21M12 FROM ARABIDOPSIS  
THALIANA CHROMOSOME 1, COMPLETE SEQUENCE. ;, mRNA sequence.

ACCESSION AI561100  
VERSION AI561100.1 GI:4511441

KEYWORDS EST.  
SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS 1 (bases 1 to 731)

## TITLE

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

## JOURNAL

## COMMENT

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
Insert Length: 2047 Std Error: 0.00  
Seq primer: 40UP from Gibco  
High quality sequence stop: 367  
POB7A=No.

FEATURES  
source

Location/Qualifiers  
1. .731  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2209938"  
/clone\_lib="NCI CGAP Utl1"  
/tissue\_type="well-differentiated endometrial  
adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.75 kb. Life Technologies catalog #:  
11538-014"

BASE COUNT 180 a 172 c 154 g 224 t 1 others  
ORIGIN

Query Match 11.8%; Score 239.4; DB 1; Length 731;  
Best Local Similarity 70.6%; Pred. No. 2.7e-50;  
Matches 360; Conservative 0; Mismatches 147; Indels 3; Gaps 3;

QY 665 GTGTGTTTCATCATCAAGAGCTACTCTGAGGACGACATCCACCGCTCCATTAGTACTCCA 724  
DB 688 GGGTTTTTCATCATTCAGGCGCACTCTAGGAGCATATCCCGCTCCCATTAAGTA-TATA 630  
QY 725 TCTGTGTAGCAGACAGCAGCGCAACAAGCGCTGTGACAGCGCTTCCGCTGCATGACGA 784  
DB 629 TTGGGTGACAGCAGAGCATGTACAGAGACTGGATGCTGTATCGTTCCCATGATCG 570  
QY 785 GC-AAGGGGCCGCTCTACCTGCTCTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGGTG 843  
DB 569 GGAAGGGGCCGCTTTACTTTACTTTTTCAGTGTCCACGACAGTTTGGACACTTCTGTGGCGTG 510  
QY 844 GCGGAGATCAAGTCCCGCTGGAAGTACGACAGCGCGGGTCTGGTCTCAGGACAAG 903  
DB 509 GCAGAAATGAAATCTCTGTGCACTACAAACATGTGCAAGGTGTGGTCCCAAGGACAA 450  
QY 904 TGAAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGATGTACCAATTAACCACTC 963  
DB 449 TGGCAGGGTCTGTTTGTATGTCTAGGTGGATTTTGTGAAGGACGTTCCTCAATGCCA 390  
QY 964 CGGCACATCAGGCTGGAGAAATACGACAAACCGGTGCACAACTCCCGGGGACACCCAG 1023  
DB 389 CGACACATTCGCTAGAGAAACAGAGAAATAAACCACTGACCACTCTAGGGACACTCAG 330  
QY 1024 GAGTCCCTTAGAAAAAGCCAGCAAGTGTCTGAAAATATTCAGTTCTTCTACAGCACACA 1083  
DB 329 CAAGTCCCTCTGAAAAGGCTAAGCAGGTGTGAAAATATATAGCCAGCTACAGCACACC 270  
QY 1084 ACCTCCATCTTCGACCACTTTGCTCTACTACGAAAGCGCC-AGAGGAGGAGGAGGTGTG 1142  
DB 269 ACTTCCATTTTGTATGACTTCTCAGACTATGACAGCCGACAGGAGGAGAAAGTGT 210  
QY 1143 CGCAAGGAACGGCAGAGTCCGAAACAAACAA 1172  
DB 209 AAAAAGGAACGTCAAGGTCTGTGGAAATAA 180

RESULT 87  
AL628271

LOCUS 637 bp mRNA linear EST 02-NOV-2001  
DEFINITION AL628271 XGC-gastrula Silurana tropicalis cDNA clone TGas009e16 5',  
mRNA sequence.  
ACCESSION AL628271  
VERSION AL628271.1 GI:16597754  
KEYWORDS EST.

SOURCE western clawed frog.  
ORGANISM *Silurana tropicalis*  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
Xenopodinae; *Silurana*.  
1 (bases 1 to 637)  
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.  
Sanger Xenopus tropicalis EST project 2001 (10\_2001)  
Unpublished (2001)  
Contact: Huckle E  
Sanger Centre  
Hinxton, Cambridgeshire, CB10 1SA, UK  
Email: tropesanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS SEQUENCE ID: TCas009e16.sp6  
Sequencing primer: SP6  
This sequence is from a Xenopus Gene Collection (XGC) library  
constructed by Aaron M. Zorn.

TITLE  
JOURNAL  
COMMENT

REFERENCE  
AUTHORS  
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.  
Unpublished (2001)  
Contact: Huckle E  
Sanger Centre  
Hinxton, Cambridgeshire, CB10 1SA, UK  
Email: tropesanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS SEQUENCE ID: TCas009e16.sp6  
Sequencing primer: SP6  
This sequence is from a Xenopus Gene Collection (XGC) library  
constructed by Aaron M. Zorn.

FEATURES  
source  
1..637  
/organism="Silurana tropicalis"  
/db xref="taxon:8364"  
/clone="TCas009e16"  
/clone\_lib="XGC-gastrula"  
/dev\_stage="gastrula (stages 10.5-13 mixed)"  
/lab\_host="Escherichia coli XL1-blue"  
/notes="Vector: PCS107; Site 1: EcoRI; Site 2: NotI; cDNA  
was oligo dT primed from Sug of poly A+ RNA from stages  
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated  
into PCS107 with EcoRI at the 5' end and NotI at the 3'  
end."

BASE COUNT 165 a 165 c 144 g 163 t

ORIGIN  
Query Match 11.8%; Score 239; DB 1; Length 637;  
Best Local Similarity 71.5%; Pred. No. 3.3e-50;  
Matches 314; Conservative 0; Mismatches 125; Indels 0; Gaps 0;  
QY 583 GAATCCCAACCCCGCTTGAAGAACTGAAGGCTCTCAGACTACACCCGAAAGAGTTT 642  
DB 199 GAGCTCACCCTGCTTGGAGAAATGGTTCCTCAACACTACATCCCAAGACTTT 258  
QY 643 GAGTGGAACTGAAAGCGGCGTGTTCATCATCAAGAGCTACTCTGAGGACGACATC 702  
DB 259 GACTTCAGCCTTAAACTTGGTCGGGTGTTCAATGTAAAGAGCTATTGAGAGATGACATT 318  
QY 703 CACCGCTCCATTAGTACTCCATCTGCTGTAGCAGAGCAGCGCAACAGCGCTGAC 762  
DB 319 CACCGCTCCATCAAGTACAATGTTTGGTGTCTTACAGAGCATGGTAACAAGCGCTGGAT 378  
QY 763 AGCGCTTCGCTGCATGAGCAGCAAGGGCGCTCTACCTGCTCTTCAGCGTCAATGGG 822  
DB 379 GCAGCTTATCGCTCTTATGGCAAGGTCCACTTACCTGCTTTTAGTGTAAATGGT 438  
QY 823 AGTGGGCATTTTGTGGGGTGGCCGAGATGAAGTCCCGTGGACTACGGCACCAGTGC 882  
DB 439 AGTGGCCACTTCTGTGGAGTTGCAGAAATGGCTCAGCAGTAGACTATATACTTTGGCG 498  
QY 883 GGGTCTGGTCTCAGGACAGTGAAGGGAGAGTTTGAATGCTCAGTGGATTTTGTGAAG 942  
DB 499 GGAGTTTGGTTCACAGGACAAATGGAAGGGCGCTTTGATGTGCGCTGGCTTTTGTCAAG 558  
QY 943 GATGTACCCCAATACAGCTCCGGCAGATCAGGCTGGAGAAATACGACAAACACCGGTC 1002  
DB 559 GATGTACTATGGACAGTTTACGTACATTCGTCTAGAGAACATGAAACAGCCAGTC 618  
QY 1003 ACAAACTCCGGGACACCC 1021  
DB 619 ACCAACTCTCGGACACAC 637  
RESULT 88  
AW767145

LOCUS AW767145 568 bp mRNA linear EST 16-FEB-2001  
DEFINITION da63d11.y1 Harland stage 19-23 *Xenopus laevis* cDNA clone  
IMAGE:3199605.5', mRNA sequence.  
ACCESSION AW767145  
VERSION AW767145.1 GI:7699143  
KEYWORDS EST.  
SOURCE African clawed frog.  
ORGANISM *Xenopus laevis*  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
Xenopodinae; *Xenopus*.  
1 (bases 1 to 568)  
Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,  
Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person,  
B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,  
Waterston, R. and Wilson, R.  
WashU Xenopus EST project, 1999  
Unpublished (1999)  
Contact: Sandy Clifton, Ph.D.  
WashU Xenopus EST project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Library constructed by R. Harland, PhD (University of California,  
Berkeley)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: Xenopus clones from this library are available  
through the I.M.A.G.E. Consortium/LLNL at:  
image.llnl.gov/image/html/iresources.shtml  
Seq primer: -40RP from Gibco  
High quality sequence stop: 486.

FEATURES  
source  
1..568  
/organism="Xenopus laevis"  
/db xref="taxon:8355"  
/clone="IMAGE:3199605"  
/clone\_lib="Harland stage 19-23"  
/tissue\_type="neurula"  
/dev\_stage="stage 19-23"  
/lab\_host="DH10B (phage-resistant)"  
/notes="Vector: PCS107 (custom); Site 1: NotI; Site 2: SalI  
; cDNA made by oligo-dT priming. Library constructed by  
Dr. Francesca Mariani in the laboratory of R. Harland,  
Ph.D. (University of California, Berkeley). References:  
XBF-2 is a transcriptional repressor that converts  
ectoderm into neural tissue. Mariani, FV. Harland, RM.,  
Development. 1998 Dec;125(24):5019-31. PMID: 9811586; UI:  
99030283; Use of large-scale expression cloning screens in  
the *Xenopus laevis* tadpole to identify gene function.  
Grammer TC, Liu XJ, Mariani FV, Harland RM., Dev Biol.  
2000 Dec 15;228(2):197-210. PMID: 1111324; UI: 20564075;  
Note: This is a Xenopus Gene Collection (XGC) library."

BASE COUNT 128 a 196 c 119 g 125 t

ORIGIN  
Query Match 11.7%; Score 237.4; DB 2; Length 568;  
Best Local Similarity 80.8%; Pred. No. 8.1e-50;  
Matches 277; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
QY 1 CAAAAGGACAAAGATAATAAAGTCAAAATGGTTCGTTTACATCAGAAGTACAGTTTCATG 60  
DB 226 CAAAGGACAAAGACAGTAAGAATTCMAAACGGATCCCTGCATCAGAGGACAGCGTGACG 285  
QY 61 ACAATGACTTTGAGCCCTACCTTACTTGGACAGTCAATACAGAGTAACAGTTACCCCTCAA 120  
DB 286 ATAATGACTTTGAGCAGTACCTGTGCGGGCAGTCCAATCAGAGTAACAGTACCCCTCCA 345  
QY 121 TGAGCGACCCCTACCTGTCCAGCTATATACCGGGGCTCATTTGGATTCTTACTCTCTCA 180  
DB 346 TGACAGACCCCTTATCTATCCAGTTACTACCCCTCTCTTATTTGGCTTTTCCTGATTCCTCA 405



kidney, heart, spleen, ovary, and muscle. The UI-R-EI library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C0) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-A1 and UI-R-EI clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-A1 and UI-R-EI library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C0 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).

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BASE COUNT      125 a      89 c      106 g      91 t
ORIGIN

Query Match      11.5%; Score 233.2; DB 1; Length 411;
Best Local Similarity 75.7%; Pred. No. 8.7e-49;
Matches 289; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 743 ACGCAACAGCGCTGACAGCGCTTCGCTGATGAGCAGCAAGGGCCGCTTACC 802
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
9 AAGGTAACAAGAGACTGGATGCCGCTATCTGTTCCATGAACGGGAAGGTCCTGTACT 68

QY 803 TGCTCTCAGCGTCAGCGGAGTGGGCAATTTTCTGGGGTGGCGAGATGAAGTCCCCG 862
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
69 TACTTTTCAGTGTCAACGGCAGTGGACATCTCTGTGGAGTTCAGAGATGAATCTGCTG 128

QY 863 TGGACTACGCGCAGTCGCGGGTCTGGTCTCAGGACAAGTGAAGGGGAAGTTTGATG 922
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
129 TGGACTACAACACATGTGCAGGTGTGTGGTCCAGGACAAATGCAATGCAAGGTCGTTTGACG 188

QY 923 TCCAGTGGATTTTGTAAAGATGTACCAATAACAGTCTCCGCAATCAGGCTGGAGA 982
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
189 TCAGATGGATTTTGTGAAGACGCTTCCCAATAGCAACTCGCACACATTCGTCTAGAGA 248

QY 983 ATACGACAACAACCGGTCAAACTCCGGGACACCCAGAGGTGCCCTTAGAAAAAG 1042
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
249 ACAACGAGATTAACAGTGAACCACTCTAGGACATCTCAGGAAGTGCCTCTGGAAGAAG 308

QY 1043 CCAAGCAAGTGTCTGAAATATCAGTTCTTACAGCACACAACTCCATCTTCGACGACT 1102
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
309 CTAAGCAGGTGTTTGAATATCATGCCAGCTACAGCACACACCTTCATTTTGTATGACT 368

QY 1103 TTGCTCTACGAGAGAGGCCA 1124
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
369 TCTCACACTATGAGAAACGCCA 390

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RESULT 91
AW276263/c      605 bp      mRNA      linear      EST 03-JAN-2000
LOCUS      xr08h12.x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:2759591.3,
DEFINITION      similar to TR:064526 O64526 YUP8H12R.13 PROTEIN. ;, mRNA sequence.
ACCESSION      AW276263
VERSION      AW276263.1 GI:6683293
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 605)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL      Tumor Gene Index
COMMENT      Unpublished (1997)
Contact: Robert Straubeberg, Ph.D.

```

Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: -40UP from Gibco  
High quality sequence stop: 428.

#### FEATURES

```

source
1..605
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2759591"
/clone_lib="NCI CGAP Lu28"
/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."
BASE COUNT      142 a      146 c      122 g      193 t
ORIGIN

```

```

Query Match      11.5%; Score 232.8; DB 2; Length 605;
Best Local Similarity 73.0%; Pred. No. 1.2e-48;
Matches 311; Conservative 0; Mismatches 114; Indels 1; Gaps 1;

QY 748 AACAGCGCTGACAGCGCTTCGCTGATGAGCAGCAAGGGCCGCTTACCTGCTC 807
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
605 AACAGAGACTGGATGCTGCTNATCGTTCATGAACGGGAAGGCCCGTTTACTTCTT 546

QY 808 TTACGCTCAATGGGAGTGGGCAATTTTGTGGGTGGCGAGATGAAGTCCCCGCTGAC 867
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
545 NTCAGTGTCAACGGCAGTGGACACTTCTGTGGCGTGGCAGAAATGAATCTGCTGTGAC 486

QY 868 TAGCGCACAGTGC CGGGTCTGCTCTCAGGACAAGTGGGAAGGAAAGTTTGATGTCCAG 927
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
485 TACAACACATGTGCAGGTGTGTGGTCCCAGGACAAATGGAAGGGTCTGTTTGTGTCAGG 426

QY 928 TGGATTTTCTTAAGATGTACCAATAACAGTCCGGCACATCAGGCTGGAGAATAAC 987
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
425 TGAATTTTGTGAAGAGACGTTCCTCAATAGCCAACTTGGACACATTCGCCCTAGAGAACAC 366

QY 988 GACAAACAAACCGGTCAAACTCCCGGACACCCAGGAGTGGCCTTAGAAAAAGCCAAAG 1047
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
365 GAGATTAACACAGTGCACCACTCTAGGACACTCAGGAAGTGCCTCTGGAAGGCTAAG 306

QY 1048 CAAGTGTGAAATATCAGTTCTCTACAGCACACAACTCCATCTTTCGACGACTTTGCT 1107
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
305 CAGGTGTGAAAAATATAGCCAGCTACAGCACACCACTTCCATCTTTGTGACTTCTCA 246

QY 1108 CACTACGGAAGCGCC-AGAGGAGGAGGAGTGTGTCGCGAGGACGCAAGTCTGGAAC 1166
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
245 CACTATGAGCCACGCCAAGAGGAACAAGAAAGTGTAAAAAAGGAACGTCGAGGTCTGGG 186

QY 1167 AACAA 1172
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
185 AATAA 180

```

```

RESULT 92
BB625167
LOCUS      BB625167
DEFINITION      BB625167 RIKEN full-length enriched, adult male cecum Mus musculus
ACCESSION      BB625167
VERSION      BB625167.1 GI:16463485
KEYWORDS      EST.
SOURCE      house mouse,
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```











```
/clone_lib="Soares_mammary_gland_NMLMG"
```

```
/sex="Female (lactating)"
```

```
/tissue_type="mammary gland"
```

```
/lab_host="DH10B"
```

```
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from mammary  
gland tissue from a lactating female, and was then primed  
with a Not I - oligo(dT) primer. Double-stranded cDNA was  
ligated to Eco RI adaptors (Pharmacia), digested with Not  
I and cloned into the Not I and Eco RI sites of the  
modified pT7T3 vector. Library is normalized. Library  
was constructed by Bento Soares and M. Fatima Bonaldo."
```

```
BASE COUNT      146 a  146 c  119 g  190 t
ORIGIN
Query Match      11.1%; Score 225.2; DB 2; Length 601;
Best Local Similarity 73.3%; Pred. No. 1.1e-46;
Matches 315; Conservative 0; Mismatches 113; Indels 2; Gaps 2;
```

```
Qy 750 CAAGCGCTGGACAGCGCTTCCGCTGCATGAGCAGCAAGGGGCCGCTTACCTGCTTT 809
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 601 CAAGAGACTGGATCGCGCTATCG-TCCATGAATGGGAAGGTCCTGTTACTTACTTTT 543
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 810 CAGCGTCAATGGGATGGGCATTTTGTGGGTGGCCGAGATGAATCCCGTGGACTA 869
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 542 CAGTGTCAACGGCAGTGGACACTTCTGTGGAGTTGCAGAGATGAATCTGCTGGACTA 483
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 870 CGGCACAGTCCCGGGTCTGCTCTCAGGACAAAGTGGGAAGGGAAGTTGTATGCCAGTG 929
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 482 CAACACATGTCAGGTGTGTGGTCCAGGACAAATGGNAGGTCGTTGATGTCAATG 423
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 930 GATTTTGTAAAGATGTACCCAAATACCAAGCTCCGGCACATCAGGCTGGGAATACGA 989
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 422 GATTTTGTGAAGACGTTCCCAATAGCCAACTCGGCACTCAGGAAGTGCCTGGAAAAGCTAAGCA 363
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 990 CAACAAACCGGTCACAACTCCCGGGACACCCAGAGGTGCGCTTAGAAAAGCCAGCA 1049
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 362 GAATAAACCAAGTGAACCAACTTGGGACACTCAGGAAGTGCCTGGAAAAGCTAAGCA 303
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1050 AGTCTGAAAATATCAGTTCTCTCAAGCACACCACTCCATCTTCAGACGACTTTGTCTCA 1109
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Db 302 GGTGTTGAAAATCATAGCCACTACAGCACACCACTTCCATTTTGTATGACTTCTACA 243
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1110 CTACGAGAAGCCGC-AGAGGAGGAGGAGTGTGTCGCAAGAACCGGAGAGTCGAAAACAA 1168
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Db 242 CTATGAGAAACGCCAAGAGGAAGAAAGTGTAAAAAGCAACGTCAAGTCTGTGGAA 183
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1169 ACAATGAGGG 1178
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 ATAGAAAGCG 173
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```

```
RESULT 98
AW535358/c      597 bp  mRNA  linear  EST 06-MAR-2000
LOCUS           UI-R-BS0-aoc-c-04-0-UI.s1 UI-R-BS0 Rattus norvegicus cDNA clone
DEFINITION      UI-R-BS0-aoc-c-04-0-UI 3', mRNA sequence.
ACCESSION       AW535358
VERSION         AW535358.1 GI:717772
KEYWORDS        EST.
SOURCE          Norway rat.
ORGANISM        Rattus norvegicus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                Rattus.
REFERENCE       1 (bases 1 to 597)
AUTHORS        Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE          Normalization and subtraction: two approaches to facilitate gene
                discovery
JOURNAL        Genome Res. 6 (9), 791-806 (1996)
MEDLINE        97044477
COMMENT         Contact: Soares, MB
                Program for Rat Gene Discovery and Mapping
```

```
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized ovary library cDNA Library Preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
```

```
FEATURES
Location/Qualifiers
source          1..597
                /organism="Rattus norvegicus"
                /strain="Sprague-Dawley"
                /db_xref="taxon:10116"
                /clone="UI-R-BS0-aoc-c-04-0-UI"
                /clone_lib="UI-R-BS0"
                /dev_stage="embryonic 13 dpc"
                /lab_host="DH10B (Life Technologies)"
                /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BS0
                library is derived from 13 dpc whole embryo tissue. For a
                detailed description of the library from which this clone
                was derived, please visit our web site at
                ratcst.eng.uiowa.edu.
                TAG LIB=UI-R-BS0
                TAG TISSUE=ovary
                TAG SEQ=TCAC"
```

```
BASE COUNT      141 a  142 c  114 g  200 t
ORIGIN
Query Match      11.1%; Score 224.8; DB 2; Length 597;
Best Local Similarity 73.5%; Pred. No. 1.3e-46;
Matches 300; Conservative 0; Mismatches 107; Indels 1; Gaps 1;
```

```
Qy 772 CGCTGCATGACGACGAGGGCCGCTCTACTGCTCTTCAGCGTCATGGAGTGGGCAT 831
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 596 CGTTCATGAACGGGAAGGGTCCGCTACTTACTTTTTCAGTTTCACCGGAGTGGACAC 537
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 832 TTTTGTGGCGTGGCCGAGATGAAGTCCCCGCTGGACTACGGCACAGTGCCTGGGCTCTGG 891
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 536 TTCTGTGGAGTTGCAGAGATGAATCTGCTGTGGACTACACACATGTGCAGGTGTGG 477
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Qy 892 TCTCAGCAAGTGGAAAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGGATGTACCC 951
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Db 476 TCCAGGACAAATGGNAGGTCGTTTTTGACGTCAGATGGATTTTGTGAAGGACGTTCCC 417
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Qy 952 AATNACAGCTCCGGACATCAGCTGGAGATAACGACAAACACCGGTCACAAACTCC 1011
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Db 416 AATAGCCAACTGGACACATTCGCTTAGAAGAACCAACGAGAATAAACCACTGACCACTCT 357
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Qy 1012 CGGACACACCAGAGGTGCCCTTAGAAAAAGCCAAGCAAGTGTGAAAAATATCAGTTCC 1071
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Db 356 AGGACACTCAGNAGTGCCTCTGAAAAAGCTTAAGCAGGTGTTGAAAATCATAGCCAGC 297
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Qy 1072 TACAAGCACAAACCTCCATCTTTTCGACGACTTTGCTCCTACACGAGAACGCC-AGAGGAG 1130
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Db 296 TACAAGCACACCACTTCCATTTTGTATGACTTCTTCACACTATGAGAAACGCCAAGAGGAA 237
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1131 GAGGAGTGTGGCAAGGAACCGCAGAGTCGAAACAAACAATGAGGG 1178
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 236 GAAGAAAGTGTAAAAAGGAACGTCAGGCGCTGGGAATATAAAGCG 189
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
RESULT 99
AW075266/c
LOCUS           AW075266
DEFINITION      wz96e04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:256686 3',
```

mrna sequence.  
ACCESSION AW075266  
VERSION AW075266.1 GI:6030264  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 232)  
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BTCAP), Tumor Gene Index  
JOURNAL Unpublished (1998)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: -40UP from Gibco  
High quality sequence stop: 222.  
Location/Qualifiers  
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1..232  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:256686"  
/clone\_lib="NCI CGAP Brn25"  
/tissue\_type="anaplastic oligodendroglioma"  
/lab\_host="PH108"  
/note="Organ: brain; Vector: pPT3D-Pac (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5',  
TGTTACCAATCGAATGCGAGCGCGATAGGTTTTTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pPT3D vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."  
BASE COUNT 91 a 51 c 41 g 49 t  
ORIGIN  
Query Match 11.0%; Score 224; DB 2; Length 232;  
Best Local Similarity 100.0%; Pred. No. 1.6e-46;  
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 232 CAATGAGGGGCAACAGTTCTTACATGTTCTAACGTTTCACCTTGAACACAGTTTAAAA 173  
QY 1230 CAGCTGTGCTGTGCTCAGCTCAGTGTGCTGCTCCGTCGCGGGGGTTCAGTGTTCATCTTT 1289  
DB 172 CAGCTGTGCTGTGCTCAGCTCAGTGTGCTGCTCCGTCGCGGGGGTTCAGTGTTCATCTTT 113  
QY 1290 GCCTTTCTGCTGTGTTGTTTGGCCAGATGATCTGCATTTATTTGATCTTTTCTATG 1349  
DB 112 GCCTTTCTGCTGTGTTTGGCCAGATGATCTGCATTTATTTGATCTTTTCTATG 53  
QY 1350 TATTATAATCCTGTAGAGTCACTATATAGAGGAGTATTTTTTT 1393  
DB 52 TATTATAATCCTGTAGAGTCACTATATAGAGGAGTATTTTTTT 9  
RESULT 100  
AW503320  
LOCUS  
DEFINITION UI-HF-BN0-akx-d-02-0-UI.r1 NIH\_MGC\_50 Homo sapiens cDNA clone  
IMAGE:3078578 5', mRNA sequence.

ACCESSION AW503320  
VERSION AW503320.1 GI:7118597  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 496)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward.  
Location/Qualifiers  
FEATURES  
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/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LTI)"  
/note="Vector: pPT3D-Pac; Site 1: NotI; Site 2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(3.5-4.4kb). Directionally cloned. Cells provided by  
Louis M. Staudt, Ph.D. Library preparation by Maria de  
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."  
BASE COUNT 170 a 87 c 109 g 130 t  
ORIGIN  
Query Match 11.0%; Score 223.4; DB 2; Length 496;  
Best Local Similarity 74.3%; Pred. No. 2.9e-46;  
Matches 295; Conservative 0; Mismatches 101; Indels 1; Gaps 1;  
QY 777 CATGACGACGAAGGGGCCGCTCTACTGCTCTTCAGCGTCAATGGAGTGGGCATTTTGG 836  
DB 1 CACGAGGGGGAAGGCCCACTCTATTACTCTTCAGTGTGAATGGCAGTGGACATTTTGG 60  
QY 837 TGGGTTGGCCGAGATGAAGTCCCGGTGGACTACGGCACACAGTGCAGGGGTCTGTCTCA 896  
DB 61 TGGAGTGGCTGAAATGAAGTCTGTTGTGGACTATAATGCGTATGCTGTGCTGTCTCA 120  
QY 897 GCACAGTGGAGGGGAAGTTTGATGTCAGTGGATTTTGTAGGATGTACCCCAATAA 956  
DB 121 GGATAGTGGAGGGGCAAAATTTGAAGTTAAATGGATCTTTGTCAAAGATGTTCCCAATAA 180  
QY 957 CCAGCTCCGGCACATCAGGCTGGAGATAACGACAAACACCGGTCAACAACTCCCGGGA 1016  
DB 181 CCATTAACGGCATATTCGCTTAGAATAATATGACAAACACCGGTACCAATTCAGGGA 240  
QY 1017 CACCCAGGAGGTGCCCTTAGAAAAAGCCAAAGAGTGTGAAAAATATCAGTTCTCTACAA 1076  
DB 241 CACTCAAGAGGTACCCCTAGAAAAAGCTAAGCAAGTCTTAAATAATTTGCTACTTTCAA 300  
QY 1077 GCACACAACCTCACTTCGACGACTTTGCTCACTACGAGAGCG-CCAGAGGAGGAGGA 1135  
DB 301 GCATACCACTCAATCTTTGATGACTTTTCACATTATGAANAACCGTCAAGAGAGGAGGA 360  
QY 1136 GTGTGGTGGCAAGACGCGCAGAGTCCGAACAAACAA 1172  
DB 361 AGCCATGCGGTAGGAGAGAAATAGAAACAAACATAA 397

Mon Mar 24 15:50:03 2003

us-09-877-633-2.rst

Page 64

Search completed: March 24, 2003, 01:32:06  
Job time : 1248 secs

GenCore version 5.1.4 p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 23, 2003, 23:43:46 ; Search time 3338 Seconds  
(without alignments)  
9839.559 Million cell updates/sec

Title: US-09-877-633-2

Perfect score: 2028

Sequence: 1 caaaaggacaagataataaa.....agtaacagacagtgtgatgga 2028

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 350 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	770	38.0	903	14	BQ677542
2	725.8	35.8	889	14	BQ682082
3	701.4	34.6	928	14	BQ421505
4	674.6	33.3	1109	12	BE894361
5	650.8	32.1	852	12	BE892982
6	648.8	32.0	1014	9	AV079675

C	7	644.6	31.8	561	9	AL574115
C	8	633.4	31.2	1068	9	AL515908
C	9	628.8	31.0	684	10	AW001012
C	10	626.6	30.9	932	10	AV726565
C	11	623.8	30.8	1479	13	BM423045
C	12	615.2	30.3	633	14	BM685329
C	13	601.8	29.7	664	10	BE646471
C	14	594.6	29.3	689	13	BG911605
C	15	583.2	28.8	600	10	AW387914
C	16	581.8	28.7	808	12	BE892829
C	17	580.4	28.6	736	13	BI091481
C	18	571	28.2	669	10	AW964022
C	19	555	27.4	582	13	BI262492
C	20	553.4	27.3	929	12	BQ249197
C	21	551	27.2	563	10	AW387761
C	22	545.6	26.9	893	12	BG216572
C	23	542.8	26.8	688	13	BM014798
C	24	519.2	25.6	837	10	BE542593
C	25	519	25.6	921	9	AL562740
C	26	512	25.2	598	14	BM931439
C	27	506.2	25.0	886	12	BG828010
C	28	503.6	24.8	659	10	AW387819
C	29	502.6	24.8	530	12	BP915645
C	30	483.6	23.8	551	10	AW387869
C	31	483.6	23.8	688	9	AJ449334
C	32	480.6	23.7	499	10	AW387916
C	33	480.4	23.7	538	17	AQ564196
C	34	476.4	23.5	964	13	BI739961
C	35	475	23.4	937	12	BF529242
C	36	472	23.3	1002	14	BQ236558
C	37	466.8	23.0	584	10	AW387858
C	38	456.8	22.5	460	9	AA976117
C	39	450	22.2	778	9	AL580786
C	40	445.2	22.0	838	9	AL524372
C	41	443.4	21.9	471	12	BG431474
C	42	442.4	21.8	614	9	AI536362
C	43	439.4	21.7	902	14	BQ421488
C	44	434.4	21.4	977	13	BM556661
C	45	431	21.3	435	14	BM745209
C	46	430.8	21.2	623	13	BI224711
C	47	426	21.0	629	14	R69898
C	48	424.4	20.9	687	13	BQ44639
C	49	423.4	20.9	449	9	AI083909
C	50	418.2	20.6	435	10	AW387755
C	51	418	20.6	429	10	AV725141
C	52	418	20.6	429	10	AV729447
C	53	418	20.6	429	10	AV729585
C	54	411.6	20.3	687	13	BQ444420
C	55	411	20.3	432	14	BM745243
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C	59	402.2	19.8	977	9	AL514504
C	60	401.8	19.8	666	10	BB068522
C	61	397.6	19.6	441	10	AW138532
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C	63	390.6	19.3	702	9	AL565188
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C	65	385.4	19.0	773	9	AL558224
C	66	384.4	18.9	772	9	AL580105
C	67	383.8	18.9	649	13	BI283897
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C	70	363	17.9	659	10	AW766504
C	71	362.6	17.8	733	13	BI254326
C	72	361.8	17.8	790	10	BE542677
C	73	360.2	17.8	674	12	BF025564
C	74	356.8	17.6	598	13	BI713733
C	75	351.4	17.3	361	14	BM828295
C	76	350.8	17.3	273	12	BE715628
C	77	348.6	17.2	658	17	CNS02421
C	78	345	17.0	701	13	BI562443
C	79	345	17.0	1010	10	BB610489

80	345	17.0	1041	14	BQ27973	AGENCOURT	BQ27973	153	272.6	13.4	639	10	AM420132
81	342.8	16.9	720	13	BQ61839	BQ61839	BQ61839	C 154	272.4	13.4	682	14	BM979382
82	342.2	16.9	706	13	BQ64834	BQ64834	BQ64834	C 155	271.4	13.4	727	12	BM979382
83	340.5	16.8	883	14	BQ23380	AGENCOURT	BQ23380	C 156	271.4	13.4	740	9	AM168034
84	339	16.7	739	17	BH53078	BH53078	BH53078	C 157	271.4	13.4	740	9	AM168034
85	338	16.7	917	9	AL515909	AL515909	AL515909	C 158	270.6	13.3	741	10	AM16778
86	336.8	16.6	355	9	AA460050	AA460050	AA460050	C 159	270.4	13.3	741	12	BF983198
87	336.2	16.6	937	14	BQ899696	BQ899696	BQ899696	C 160	269.8	13.3	741	12	BF983198
88	336	16.6	719	13	BQ63156	BQ63156	BQ63156	C 161	269.4	13.3	741	12	BF983198
89	335.6	16.5	632	10	BE026361	BE026361	BE026361	C 162	269.2	13.3	741	12	BF983198
90	335.2	16.5	873	14	BQ232423	AGENCOURT	BQ232423	C 163	267.8	13.2	741	12	BF983198
91	333.4	16.4	363	14	H63270	H63270	H63270	C 164	267.4	13.2	741	12	BF983198
92	333.4	16.4	943	14	BQ899797	AGENCOURT	BQ899797	C 165	266.8	13.2	741	12	BF983198
93	333	16.4	542	9	AA636479	AA636479	AA636479	C 166	266.4	13.1	741	14	BQ56442
94	333	16.4	694	14	BM772351	BM772351	BM772351	C 167	265.4	13.1	741	14	BQ56442
95	332	16.4	505	14	BM748094	BM748094	BM748094	C 168	265.2	13.1	741	14	BQ56442
96	327	16.1	341	9	AA361068	AA361068	AA361068	C 169	264.6	13.1	741	14	BQ56442
97	326.8	16.1	530	10	AM465429	AM465429	AM465429	C 170	263.6	13.0	741	14	BQ56442
98	324.8	16.0	411	14	N95559	N95559	N95559	C 171	263.4	13.0	741	14	BQ56442
99	323.6	16.0	695	12	BG499817	BG499817	BG499817	C 172	263.4	13.0	741	14	BQ56442
100	322.4	15.9	654	9	AL774891	AL774891	AL774891	C 173	262	12.9	741	14	BQ56442
101	321	15.8	693	17	AZ793507	AZ793507	AZ793507	C 174	262	12.9	741	14	BQ56442
102	321	15.8	713	14	BQ773021	BQ773021	BQ773021	C 175	259.4	12.8	741	14	BQ56442
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105	317.2	15.6	819	12	BE897197	BE897197	BE897197	C 178	257.8	12.7	741	14	BQ56442
106	316.4	15.6	383	10	AV711963	AV711963	AV711963	C 179	257.2	12.7	741	14	BQ56442
107	315.8	15.6	340	10	BE089793	BE089793	BE089793	C 180	257	12.7	741	14	BQ56442
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109	313.4	15.5	524	13	BM194314	BM194314	BM194314	C 182	255.6	12.6	741	14	BQ56442
110	313	15.4	373	14	W14779	W14779	W14779	C 183	255.6	12.6	741	14	BQ56442
111	313	15.4	526	13	BI449923	BI449923	BI449923	C 184	255.2	12.6	741	14	BQ56442
112	312.4	15.4	628	13	BI878624	BI878624	BI878624	C 185	254.8	12.6	741	14	BQ56442
113	311.2	15.3	749	12	BG572409	BG572409	BG572409	C 186	253.2	12.6	741	14	BQ56442
114	309	15.2	681	14	BM772372	BM772372	BM772372	C 187	249	12.3	741	14	BQ56442
115	308.8	15.2	565	12	BG86244	BG86244	BG86244	C 188	248	12.2	741	14	BQ56442
116	308	15.2	656	12	BE743585	BE743585	BE743585	C 189	246.8	12.2	741	14	BQ56442
117	307.8	15.2	780	10	AV757830	AV757830	AV757830	C 190	245.2	12.1	741	14	BQ56442
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119	306.2	15.1	754	14	BQ571766	BQ571766	BQ571766	C 192	244.4	12.1	741	14	BQ56442
120	305.8	15.1	1013	10	BE618817	BE618817	BE618817	C 193	243.8	12.0	741	14	BQ56442
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135	292.8	14.4	905	12	BE893890	BE893890	BE893890	C 208	233.2	11.5	741	14	BQ56442
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137	290.8	14.3	752	12	BF690959	BF690959	BF690959	C 210	232.8	11.5	741	14	BQ56442
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139	287.2	14.2	316	9	AA323869	AA323869	AA323869	C 212	231	11.4	741	14	BQ56442
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141	285	14.1	439	14	BM979533	BM979533	BM979533	C 214	228	11.2	741	14	BQ56442
142	284.8	14.0	616	9	AJ447891	AJ447891	AJ447891	C 215	227	11.2	741	14	BQ56442
143	284	14.0	679	9	AA977084	AA977084	AA977084	C 216	226.6	11.2	741	14	BQ56442
144	279.4	13.8	464	17	AZ906554	AZ906554	AZ906554	C 217	226.2	11.2	741	14	BQ56442
145	278.4	13.7	993	14	BQ423258	BQ423258	BQ423258	C 218	226	11.1	741	14	BQ56442
146	276.8	13.6	677	14	BQ182901	BQ182901	BQ182901	C 219	225.2	11.1	741	14	BQ56442
147	276.2	13.6	882	12	BF166918	BF166918	BF166918	C 220	225	11.1	741	14	BQ56442
148	274.8	13.6	689	9	AA398704	AA398704	AA398704	C 221	224.8	11.1	741	14	BQ56442
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151	273.2	13.5	685	14	BQ783261	BQ783261	BQ783261	C 224	223.4	11.0	741	14	BQ56442
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229	220.2	10.9	323	12	BF770536	BF770536 RC1-IT001	179.4	8.8	576	13	BJ096494	BJ096494
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231	218.8	10.8	583	9	AA100514	AA100514 z046d11.s	179.2	8.8	717	10	BS618308	BS618308 601462688
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238	214	10.6	358	9	AA632856	AA632856 n88a03.s	175.8	8.7	545	9	AL633246	AL633246
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254	205.4	10.1	542	10	AW540725	AW540725 C0136D09-	170.6	8.4	354	14	F22929	F22929 SSC16H08 Po
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267	201	9.9	520	14	N79648	N79648 y281d08.r1	167.4	8.3	745	13	BI602130	BI602130 603246251
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## ALIGNMENTS

RESULT 1  
BQ677542

LOCUS  
DEFINITION

ACCESSTION  
VERSION

KEYWORDS  
SOURCE

ORGANISM

REFERENCE

AUTHORS  
TITLE

JOURNAL

BQ677542 903 bp mRNA linear EST 15-JUL-2002  
AGENCOURT\_8212225 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6260712  
5', mRNA sequence.

BQ677542  
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EST.  
human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 903)  
NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-k@mail.nih.gov  
 Tissue Procurement: DCTD/DTF  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM2420 row: e column: 01  
 High quality sequence stop: 660.  
 Location/Qualifiers

## FEATURES

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 /lab\_hosts="DH10B (phage-resistant)"  
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:  
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 GGACAG(G). Library constructed by Ling Hong in the  
 laboratory of Gerald M. Rubin (University of California,  
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH MGC Library."  
 BASE COUNT 232 a -229 c 242 g 198 t 2 others

ORIGIN  
 Query Match 38.0%; Score 770; DB 14; Length 903;  
 Best Local Similarity 97.0%; Pred. No. 8.9e-155;  
 Matches 848; Conservative 0; Mismatches 17; Indels 9; Gaps 5;

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 Db 1 AGACCCGCTGGTGGCCCGACGACAGAAACGGCGCGTTTGGGCGAGCGGAGGGGCTG 60  
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 Qy 650 ATCTGAAAGCGGGCGTGTTCATCATCAAGAGTACTCTGAGAGCGACATCCACGCT 709  
 Db 181 ATCTGAAAGCGGGCGTGTTCATCATCAAGAGTACTCTGAGAGCGACATCCACGCT 240  
 Qy 710 CCATTAAAGTACTCTGCTGAGTACGACAGAGCGGCAACAGCGCTGACAGCGCT 769  
 Db 241 CCATTAAAGTACTCTGCTGAGTACGACAGAGCGGCAACAGCGCTGACAGCGCT 300  
 Qy 770 TCCGCTGATGAGCAGGAGCGGCGCTTCTACCTGCTCTTCCAGGCTCAATGGGAGTGGGC 829  
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 Qy 890 GGTCTCAGGACAAT-GGAAGGGAGTTTGTATGTCAGTCCAGTGGATTTTGTAAAGGATGA 948  
 Db 421 GGTCTCAGGACAATGGAAGGGAGTTTGTATGTCAGTCCAGTGGATTTTGTAAAGGATGA 480  
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 RESULT 2  
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 LOCUS  
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 VERSION BQ682082.1  
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 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 889)  
 AUTHORS NIH-National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-k@mail.nih.gov  
 Tissue Procurement: DCTD/DTF  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLCM2426 row: f column: 01  
 High quality sequence stop: 567.  
 Location/Qualifiers  
 1. .889  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6263040"  
 /clone\_lib="NIH\_MGC\_112"  
 /tissue\_type="melanotic melanoma, cell line"  
 /lab\_hosts="DH10B (phage-resistant)"  
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dr priming. Directionally cloned  
 into EcoRI/XhoI sites using the following 5' adaptor:  
 GGACAG(G). Library constructed by Ling Hong in the  
 laboratory of Gerald M. Rubin (University of California,  
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH MGC Library."  
 BASE COUNT 223 a -238 c 248 g 178 t 2 others  
 ORIGIN  
 Query Match 35.8%; Score 725.8; DB 14; Length 889;  
 Best Local Similarity 97.0%; Pred. No. 2.7e-145;  
 Matches 781; Conservative 0; Mismatches 19; Indels 5; Gaps 4;

Qy 470 AGACCCGCTGGTGGCCCGACGACAGAAACGGCGCGTTTGGGCGAGCGGAGGGGCTG 529



Db 1 AGACCCCGCTGGGTGGCCCGACGACAGAAACCGCGCTTTGGGCAGAGCGGAGGGCTG 60  
QY 530 GCAGCGATAGCAACTCTCTCTGGAACGCTCAGAGCTTAATCTGCCCCCAGCGGTGCAATCCC 589  
Db 61 GCAGCGATAGCAACTCTCTCTGGAACGCTCAGAGCTTAATCTGCCCCCAGCGGTGCAATCCC 120  
QY 590 ACCCGCTCTTGAAGAACTGAAGGCTGCTCAGAGCTAACAACCCGAAAGATTTGAGTGA 649  
Db 121 ACCCGCTCTTGAAGAACTGAAGGCTGCTCAGAGCTAACAACCCGAAAGATTTGAGTGA 180  
QY 650 ATCTGAAGCGGGCGGTGTTTATCATCAAGAGCTACTCTGAGGACGACATCCACGCT 709  
Db 181 ATCTGAAGCGGGCGGTGTTTATCATCAAGAGCTACTCTGAGGACGACATCCACGCT 240  
QY 710 CCATTAAGTACTTCCATCTGCTGTAGCAGACAGCAGCGCAACAACGCGCTGACAGCGCT 769  
Db 241 CCATTAAGTACTTCCATCTGCTGTAGCAGACAGCAGCGCAACAACGCGCTGACAGCGCT 300  
QY 770 TCCGCTGCATGAGCAGCAAGGGGCCCTTACTCTGCTCTTTCAGCGTCAATGGGAGTGGC 829  
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QY 830 ATTTTGTGGGTGGCCGAGATGAAGTCCCGCTGGACTAGGACACGAGTCCCGGTCT 889  
Db 361 ATTTTGTGGGTGGCCGAGATGAAGTCCCGCTGGACTAGGACACGAGTCCCGGTCT 420  
QY 890 GGTCTCAGGACAACTGCAAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGATGTAC 949  
Db 421 GGTCTCAGGACAACTGCAAGGGGAAGTTTGATGTCAGTGGATTTTGTAAAGATGTAC 480  
QY 950 CCAATAACCAAGCTCCGCGACATCAGGCTGGAGATAACGACAAACAAACCGGTCAAACT 1009  
Db 481 CCAATAACCAAGCTCCGCGACATCAGGCTGGAGATAACGACAAACAAACCGGTCAAACT 540  
QY 1010 CCGGGACACCCAGGAGGTGCTTGAAGAAAGCAAGCAAGTCTGAAATATCATGTT 1069  
Db 541 CCGGGACACCCAGGAGGTGCTTGAAGAAAGCAAGTCTGAAATATCATGTT 598  
QY 1070 CCTTACAGCACACAACTCCATCTCCAGCAGCTTTGCTCACTACGAGCGCA--GAG 1127  
Db 599 CCTTACAGCACACAACTCCATCTCCAGCAGCTTTGCTCACTACGAGCGCAAGG 658  
QY 1128 GAGGAGAGGTGTGCGCAAGAAACGGCAGAGTGAACAAACAAATGAGGCGCAACAGT 1187  
Db 659 AAGGAGGAGTGTGCGCAAGAAACGGCAGAGTGAACAAACAAATGAGGCGCAACAGT 717  
QY 1188 TTCTTACATGTTCTAAAGTTTGAATTTGAAGAAACAGTTTAAACACAGTGTGCTGTCAGC 1247  
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QY 1248 TCCAGTGTGCTCCCGTGGGGG 1272  
Db 778 TCCCGTGGGGGNTCCCCCGGGGG 802

RESULT 3  
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LOCUS  
DEFINITION BO421505 928 bp mRNA linear EST 23-MAY-2002  
5', mRNA sequence.  
ACCESSION BO421505  
VERSION BO421505.1 GI:21116820  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 928)  
REFERENCE  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DRP/Gazdar  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
cDNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM13234 row: g column: 22  
High quality sequence stop: 578.

FEATURES  
source

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/tissue\_type="large-cell carcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: lung; Vector: pCMV-Sport6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.8 kb. Library constructed by Life  
Technologies."

BASE COUNT 243 a 230 c 233 g 221 t 1 others  
ORIGIN

Query Match 34.6%; Score 701.4; DB 14; Length 928;  
Best Local Similarity 98.0%; Pred. No. 4.6e-140;  
Matches 732; Conservative 0; Mismatches 11; Indels 4; Gaps 2;

QY 573 CCCACGGTGAATCCACCCCGTCTTGAAAACTGAAGGCTGCTCAGAGCTACAAACC 632  
Db 12 CCCACGGTGAATCCACCCCGTCTTGAAAACTGAAGGCTGCTCAGAGCTACAAACC 71  
QY 633 GAAAGAGTTTGAAGTGAATCTGAAAGCGGGCTGTGTTTCATCATCAAGAGTACTCTGA 692  
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QY 693 GAGACGACATCCACCGCTCCATTAAGTACTCTCATCTGGTGTAGCAGAGCACGGCAACAA 752  
Db 132 GAGACGACATCCACCGCTCCATTAAGTACTCTCATCTGGTGTAGCAGAGCACGGCAACAA 191  
QY 753 GCGCTTGACAGCGCTTCCGCTGCATGAGCAGCAAGGGCCGCTTACCTGCTCTTCAG 812  
Db 192 GCGCTTGACAGCGCTTCCGCTGCATGAGCAGCAAGGGCCGCTTACCTGCTCTTCAG 251  
QY 813 CGTCAATGGAGTGGGCATTTTGTGGGTGGCGGAGATGAAGTCCCGCTGGACTACGG 872  
Db 252 CGTCAATGGAGTGGGCATTTTGTGGGTGGCGGAGATGAAGTCCCGCTGGACTACGG 311  
QY 873 CACAGTGC CGGGGTCTGGTCTCAGGACAAAGTGGAAAGGGAAGTTTGTATGTCAGTGGAT 932  
Db 312 CACAGTGC CGGGGTCTGGTCTCAGGACAAAGTGGAAAGGGAAGTTTGTATGTCAGTGGAT 371  
QY 933 TTTTGTTAAGATGTATCCAAATTAACCGCTCCGCGACATCAGCGTGGAGATAACGACAA 992  
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QY 993 CAAACCGTGCACAACTCCCGGACACCCAGGAGTGGCCCTTAGAAAAAGCCCAAGCAAGT 1052  
Db 432 CAAACCGTGCACAACTCCCGGACACCCAGGAGTGGCCCTTAGAAAAAGCCCAAGCAAGT 491  
QY 1053 GCTGAAAAATATCAGTTCTTACAGCACAACCTCCATCTTCGACGACTTTGTCTCACTA 1112  
Db 492 GCTGAAAAATATCAGTTCTTACAGCACAACCTCCATCTTCGACGACTTTGTCTCACTA 551  
QY 1113 CGAAGAGCGCA--GAGAGAGGAGGTGGTGGCAGAGAAACGCGAGAGTGGAAACAAACA 1171  
Db 552 CGAAGAGCGCA--GAGAGAGGAGGTGGTGGCAGAGAAACGCGAGAGTGGAAACAAACA 611  
QY 1172 ATGAGGCGCAACAGTTTCTTACATGTTCTTAACGTTTGTGCTTTGAAACAGTTTAAACA 1231  
Db 612 ATGAGGCGCAACAGTTTCTTACATGTTCTTAACGTTTGTGCTTTGAAACAGTTTAAACA 671





adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pMT3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Patima Bonaldo."

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BASE COUNT      266 a      238 c      252 g      256 t      2 others
ORIGIN
Query Match      32.0%; Score 648.8; DB 9; Length 1014;
Best Local Similarity 82.2%; Pred. No. 8.6e-129;
Matches 822; Conservative 0; Mismatches 159; Indels 19; Gaps 6;
Qy 406 CCTCTCCAGACAGACCCCGCTTGGCTCAACCGGAGTATCAGAGCCCTCAGAGCCA 465
Db 19 CCTCTCCGTCNCGCCCNACCTGTGTGTC-CAGGCACAGTATCAGAGCCCTCAGAGCCA 77
Qy 466 CCCAGACCCGCTGGTGGCCCGCCACGACAGAAACGGCGGTTGGCCAGAGCGGAGG 525
Db 78 CTTCAACCCCGCTGT-TGGCTCTCGAAACAGAAATGAGCATGTGCCAGAGTGGAGG 136
Qy 526 GCTGGCAGCATAGCAACTCTCTGGAAACGTCAGAGCCCTAAATCTGCCCGCCAGGCTCGAA 585
Db 137 GCCAAGAGTACAGTAATCTGTGGAAATGCCCAACCTACTCTGCCCGAGTGTAGAA 196
Qy 586 TCCACCCCGCTCTTGAATAAATAGAGGCTGTACAGCTACACCCGAAAGAGTTTGAG 645
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Qy 646 TGGAACTGAAAGCGGCGGTGTTCATCATCAAGAGCTATCTGAGGAGCAGATCCAC 705
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Db 437 GGACATTTCTGGGTGGCAGAGTGAAGTCCCGTGGAGTATGGCAGCAGCGCTGGG 496
Qy 886 GTCTGGTCTCAGGCAAGTGAAGGGGAAGTTGATGTCCAGTGGATTTTGTGAAGAT 945
Db 497 GTCTGGTCTCAGGCAAGTGAAGGGGAAGTTGATGTGAAGTGGATTTTGTGAAGAT 556
Qy 946 GTACCCAAATACCGCTCCGGCAATCAGGCTGGAGATAACGACAAACCCGTCACA 1005
Db 557 GTGCCCAACACCGCTCCGGCAGATCAGACTGGAGATAACGACAAACCTGTCA 616
Qy 1006 AACTCCCGGACACCCAGAGGTGCCCTTAGAAAGCCAGCAAGTGTCTGAAATATC 1065
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Qy 1066 AGTTCTTACAGCACACACCTCTTCGACGACTTTGTCTACTACGAGAAGCGCA- 1124
Db 677 GCTTCTTATAGCACACACCTCTATCTTTGACGACTTTTCTCATATGAGAAGCGCAG 736
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Qy 1185 AGTTCTTACATGTCTAAACGTTTGTGACCTTTGAAACAGTGTAAACAGCTGTCTGTC 1244
Db 797 AGTTGTGTTTGTGTTAAGTGTGACTTTTGAAGAGTGTATGCTGTGGT 856
Qy 1245 AGCT-----CCAGTGTGTGCTCCCGTGGCGGGGTTGAGTGTGCTATCTTTGCT 1293
Db 857 CTGCTCCGAGTACAGTCCAGTGTGCTCTCGTGGGGGTTGATGTTGTCATCTTATCT 916
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Db 917 TTGTAG---TTCAATTTTCCAGATGATCTGCATTCATTGTA-TTTTCTATGTAAT 971
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Db 972 ATAATATTGTAGAACTCACTAATAAAGGAGTATTTGTTT 1011
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LOCUS      AL574115 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI040YK06 3
DEFINITION prime, mRNA sequence.
ACCESSION AL574115
VERSION    AL574115.1 GI:12934008
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 661)
AUTHORS   Li, W.-B., Gruber, C., Jesse, J., and Polaves, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 Evry cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES   Location/Qualifiers
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               enriched, double-stranded cDNA was digested with Not I and
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               vector. Library was normalized. Library was constructed by
               Life Technologies. Contact : Feng Liang Life Technologies,
               a division of Invitrogen 9800 Medical Center Drive
               Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
               Email : fliang@lifestech.com URL :
               http://fulllength.invitrogen.com"
BASE COUNT 119 a      179 c      178 g      181 t      4 others
ORIGIN
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Query Match      31.8%; Score 644.6; DB 9; Length 661;
Best Local Similarity 99.1%; Pred. No. 7.1e-128;
Matches 665; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
Qy 527 CTGCGCGGATACCACTCTCTGGAAACCTCGAGCGCTAATCTGCCCCCAGCGTCCAAT 586
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Qy 587 CCCACCCCGCTCTTGAATAAAGTCAAGCTCTCACAGCTACAACCCGAAAGAGTTTGA 646
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Qy 647 GGAATCTGAAAAGCGGCGGTGTTCATCATCAAGAGCTACTCTGAGGACGACATCCACC 706
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Qy 707 GCTCCATTAGTACTCCATCTGGTGTAGCAGAGCAGCGCAACAGCGCTCGACAGCG 766
Db 481 GCTCCATTAGTACTCCATCTGGTGTAGCAGAGCAGCGCAACAGCGCTCGACAGCG 422
Qy 767 CTTTCCGCTGCATGAGCAGCAAGGGGCCGCTCTACCTGCTCTTCAGCGTCAATGGGAGT 826
Db 421 CTTTCCGCTGCATGAGCAGCAAGGGGCCGCTCTACCTGCTCTTCAGCGTCAATGGGAGT 362
Qy 827 GGCATTTTGTGGGTGGCGGAGATGAAGTCCCGCGTGGAGTCCCGCCAGCCAGTCCCGGG 886
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Db 361 ATTGTATTTTCTGTAGACAGATAACTCTTAATTTTCAATTTTGGCAGACACTTTNTT 420
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Db 421 TTTTATTTTGGAAATCTTTCTTCCAGATCTGTGTCCTCCACTGAACACCAACCCGTCCTC 480
QY 1809 ACTGTCCTGGTCCGATTTGGGTCGATGGTGTGGGTCATGATGTGGAGGAATGGA 1868
Db 481 ACTGTCCTGGTCCGATTTGGGTCGATGGTGTGGGTCATGATGTGGAGGAACCTGG 540
QY 1869 AGGTGCTTTAGGTCCTGGTCAGGTCGGCATCTTTGTTGTCACATCTTTTAAAT 1928
Db 541 ACCTGCTTTAGTCTCGTTCAGGTCGGCATCTTTGTTGTCCTT-CACATCTTTTAC-A 598
QY 1929 TTTTACACCTTTTCTTAAGAAATCTTAATGCGCTCTTAAGTTTATACCAATAATGCTGAG 1988
Db 599 TTTTACACCTTTTCTTAAGAAATCTTAATGCGCTCTTAAG-TTTTATACCAATAATGCTGAG 657
QY 1989 CTTTAAAGTGTAGGATCTGTGTAGTACAGACAGTGTGATGGA 2028
Db 658 CTTTAAAGTGTAGGATCTGTGTAGTACAGACAGTGTGATGGA 697

RESULT 11
BM423045
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
rhesus monkey.
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheinae; Macaca.
REFERENCE
1 (bases 1 to 1479)
Katze, M.G., Bumgarner, R., Korth, M., Feldman, R., Amjadi, M. and
Holzman, T.
TITLE
Expressed sequence tags from Rhesus macaque spleen
JOURNAL
Unpublished (2002)
COMMENT
Contact: Holzman T
Katze Lab
University of Washington
Box 358070, Seattle, WA 98195-8070, USA
Tel: 206 732 6156
Fax: 206 732 6055
Email: ted@locke.hs.washington.edu
PLAYEL_D11 1479 bases; 23.2 mean phred score.

FEATURES
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BASE COUNT 561 a 342 c 359 g 217 t
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Query Match 30.8%; Score 623.8; DB 13; Length 1479;
Best Local Similarity 93.9%; Pred. No. 1.9e-123;
Matches 660; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

QY 467 CCAGACCCGCTGGTGGTCCCGACGCAACAGAAACGCGGCTTTGGCAGCGGAGGGG 526
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QY 706 CGCTCCATTAAGTACTCCATCTGGTGTAGCACAGACACGGCAACAAGCCCTGGGACAGC 765
Db 271 CGCTCCATTAAGTACTCCATCTGGTGTAGCACAGACACGGCAACAAGCCCTGGGACAGC 330
QY 766 GCGTCCCGCTGATGAGCAGCAAGGGGCCGCTCTACCTGCTCTTCAGCGTCAATGGGAGT 825
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QY 1066 AGTTCCTACAAGCACACAACTCCATCTTCGACGACTTTTGCTCACTACGAGAGCGCCAG 1125
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Db 691 GACGACGAGGAAGTGGTGGCAAGGAACCGCAGAGTGTGAAACAA 733

RESULT 12
BM685329
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 633)
Bonaldo, M.P., Lennon, G. and Soares, M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
COMMENT
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com).
Seq primer: M13 Reverse.

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Db 602 TTTTCTTTTCTTTTGAATAATCTTCTCTTCCA 633

RESULT 13  
BE646471/c

LOCUS  
DEFINITION  
7e87d05.x1 NCI\_CGAP CLL1 Homo sapiens cDNA clone IMAGE:3292137 3'-similar to TR:O64526 O64526 YUP8H12R.13 PROTEIN. ;, mRNA sequence.

VERSION  
BE646471

KEYWORDS  
EST.

SOURCE  
human.

ORGANISM  
Homo sapiens

REFERENCE  
1 (bases 1 to 664)

AUTHORS  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL  
Unpublished (1997)

COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 459.

FEATURES  
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/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TCTTACCAATCTGAAGTGGAGCGCGCCGATGCTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 168 a 177 c 150 g 168 t 1 others

ORIGIN

Query Match 29.7%; Score 601.8; DB 10; Length 664;  
Best Local Similarity 98.0%; Pred. No. 1.1e-118;  
Matches 641; Conservative 0; Mismatches 8; Indels 5; Gaps 3;

Qy 745 GGCAACAAGCGCTGACAGCGCTTCCGCTGCATGACGACAA---GGGGCCCGCTCTAC 801

Db 664 GGCAACAAGCGCTGACAGCGCTTCCGCTGCATGACGACAAAGGGCCCGCTCTAC 605

Qy 802 CTGCTCTTCAGCGTCAATGGAGTGGGCATTTTGTGGGGTGGCCGAGATGAAGTCCCC 861

Db 604 CTGCTCTTCAGCGTCAATGGAGTGGGCATTTTGTGGGGTGGCCGAGATGAAGTCCCC 545

Qy 862 GTGACCTACGGCAACAGTGC CGGGTCTCGTCTCAGGACAACTGGAAGGGGAGTTTGAAT 921

Db 544 GTGACCTACGGCAACAGTGC CGGGTCTCGTCTCAGGACAACTGGAAGGGGAGTTTGAAT 485

Qy 922 GTCCAGTGGATTTTCTTAAGGATGTACCAATATACCAGTCCCGACATCAGGTGGAG 981

Db 484 GTCCAGTGGATTTTCTTAAGGATGTACCAATATACCAGTCCCGACATCAGGTGGAG 425

Qy 982 AATAACGACAAACAAACCGGTTCACAACTCCCGGGACACACGAGGTGCCCTTAGAAAA 1041



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Db 424 AATAAGCAGCAACAAACCGGTCAAAATCTCCGGGACACCCAGGAGTGCCTTTAGAAAA 365
QY 1042 GCCAAGCAAGTGTGAAATATATCAGTTCTTACAAGCACACAACTCTTCTTCGACGAC 1101
Db 364 GCCAAGCAAGTGTGAAATATATCAGTTCTTACAAGCACACAACTCTTCTTCGACGAC 305
QY 1102 TTTGCTCATTACAGAGAGCGCCA-GAGGAGGAGAGTGTGCGCAAGAACCGCAGAGT 1160
Db 304 TTTGCTCATTACAGAGAGCGCCAAGGAGGAGAGTGTGCGCAAGAACCGCAGAGT 245
QY 1161 CGAAACAACAATGAGGCGCAACAGTTTC-TTACATGTTCTAACGTTTGACTTTCAAAA 1219
Db 244 CGAAACAACAATGAGGCGCAACAGTTTC-TTACATGTTCTAACGTTTGACTTTCAAAA 185
QY 1220 CAGTTTAAACACGTTGCTTGTGTCAGTCCAGTGTGTCCTCCGTCGCGGGGTTTCAGTG 1279
Db 184 CAGTTTAAACACGTTGCTTGTGTCAGTCCAGTGTGTCCTCCGTCGCGGGGTTTCAGTG 125
QY 1280 TTGCATCTTTGCCCTTCTTGTGCTGTTGATTTTTTGGCCAGATGATCTGCATTTATTTGTAC 1339
Db 124 TTGCATCTTTGCCCTTCTTGTGCTGTTGATTTTTTGGCCAGATGATCTGCATTTATTTGTAC 65
QY 1340 TTTTCTATGATATTAATCCTCTAGAGTCACTAATAAGGAGTATTTTTTTT 1393
Db 64 TTTTCTATGATATTAATCCTCTAGAGTCACTAATAAGGAGTATTTTTTTT 11

RESULT 14
BG911605
LOCUS 602812729F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4944846
DEFINITION 5', mRNA sequence.
ACCESSION BG911605
VERSION BG911605.1 GI:14292081
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 689)
JOURNAL NIH-MGC http://mgi.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M10890 row: i column: 07
High quality sequence stop: 663.
Location/Qualifiers
1. .689
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 190 a 154 c 157 g 188 t
ORIGIN
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Query Match 29.3%; Score 594.6; DB 13; Length 689;  
Best Local Similarity 97.0%; Pred. No. 3.7e-117;

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Matches 670; Conservative 0; Mismatches 14; Indels 7; Gaps 6;
QY 870 CGGCACAGTGC CGGGGTCTGTCTCAGGACAAGTGGAGGGAAGTTTGAATGTCAGTG 929
Db 1 CGGCACAGTGC CGGGGTCTGTCTCAGGACAAGTGGAGGGAAGTTTGAATGTCAGTG 60
QY 930 GATTTTGTAAAGATGTACCAATAACCAAGCTCCGGCACATCAGGCTGGAGATAACGA 989
Db 61 GATTTTGTAAAGATGTACCAATAACCAAGCTCCGGCACATCAGGCTGGAGATAACGA 120
QY 990 CAACAAACCGGTCAAAAACCTCCGGGACACCCAGGAGGTGCCCTTAGAAAAAGCCAAAGCA 1049
Db 121 CAACAAACCGGTCAAAAACCTCCGGGACACCCAGGAGGTGCCCTTAGAAAAAGCCAAAGCA 180
QY 1050 AGTGCTGAAATATATCAGTTCTTACAAGCACACAACTCCATCTTCGACGACTTTGCTCA 1109
Db 181 AGTGCTGAAATATATCAGTTCTTACAAGCACACAACTCCATCTTCGACGACTTTGCTCA 240
QY 1110 CTACGAGAAGCCCA-GAGGAGGAGGAGTGTGCGCAAGGACCGCAGAGTCGAACAA 1168
Db 241 CTACGAGAAGCCCAAGGAGGAGGAGTGTGCGCAAGGACCGCAGAGTCGAACAA 300
QY 1169 ACAATGAGGCGCAACCCAGTTTCTTACATGTTCTTAACGTTTGACTTTGAAAAACAGTTTAAA 1228
Db 301 ACAATGAGGCGCAACCCAGTTTCTTACATGTTCTTAACGTTTGACTTTGAAAAACAGTTTAAA 360
QY 1229 ACAGTGTGCTTTGGTCAGCTCCAGTGTGTCGTCGCGGGGGTTGAGTGTTCATCTT 1288
Db 361 ACAGTGTGCTTTGGTCAGCTCCAGTGTGTCGTCGCGGGGGTTGAGTGTTCATCTT 420
QY 1289 TGCCTTCTTGTGCTGATTTTGGCCAGATGATCTGCATTTATTTGACTTTTCTAT 1348
Db 421 TGCCTTCTTGTGCTGATTTTGGCCAGATGATCTGCATTTATTTGACTTTTCTAT 480
QY 1349 GTATTATAATCCTGTAGAGTCACTAATAAGGAGTATTTTTTTTGTGTCAGCTTATCAAT 1408
Db 481 GTATTATAATCCTGTAGAGTCACTAATAAGGAGTATTTCTCCCGTCAGCTTATCAAT 538
QY 1409 CAGACTGATCTAATGTAAATGTAAATGATATCTTTAAAAAACAAGCATCTAT-TTTGGCAGA 1467
Db 539 CAGACTGATCTAATGTAGATGTAGTATCTTTAAAAAACAAGCATCTATCTCTCGCAGA 598
QY 1468 AATTGTGTTCTTAAATTCAGTCAATTTGA-TATTCTGTGAGACTTCAATAT-TTCTCATCCC 1525
Db 599 AATTGTGTTCTTAAATTCAGTCAATCTCGACTATTTCTGTGACACTTTCATATGCTCTCATCCC 658
QY 1526 TTTATTG-CTTTTACCAACATAAGAAC 1555
Db 659 TTTATTGCTTTTATAGCAACATTAGAAAGC 689

RESULT 15
BG917914/c
LOCUS MR4-ST0119-071099-010-F01 ST0119 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW387914
ACCESSION AW387914
VERSION AW387914.1 GI:6892573
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 600)
JOURNAL HCGP http://www.ludwig.org.br/ORESTES
COMMENT The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
```

Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR4&t2=MR4-ST0119-071099-010-F01&t3=1999-10-07&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 581.

FEATURES

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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="ST0119"  
/dev\_stage="Adult"  
/note="Organ: stomach; Vector: puc18; Site: 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORSTES PCR (U.S. Letters Patent application  
No. 196, 716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
124 a 169 c 151 g 156 t

BASE COUNT

124 a 169 c 151 g 156 t

ORIGIN

Query Match 28.8%; Score 583.2; DB 10; Length 600;  
Best Local Similarity 99.3%; Pred. No. 1e-114;  
Matches 596; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
Qy 676 ATCAAGAGCTACTCTGAGGAGGAGATCCACCGCTCCATTAGTACTCCATCTGGTGTAGC 735  
Db 600 ATCAAGAGCTACTCTGAGGAGGAGATCCACCGCTCCATTAGTACTCCATCTGGTGTAGC 541  
Qy 736 ACAGAGCAGCGCAACAGCGCTGGACAGCGCTTCCGCTGCATGAGCAGCAAGGGGCC 795  
Db 540 ACAGAGCAGCGCATCAAGCGCTGGACAGCGCTTCCGCTGCATGAGCAGCAAGGGGCC 481  
Qy 796 GTCTACCTGCTCTTACGGCTCAATGGAGTGGGCAATTTTGTGGGTGGCGGAGATGAAG 855  
Db 480 GTCTACCTGCTCTTACGGCTCAATGGAGTGGGCAATTTTGTGGGTGGCGGAGATGAAG 421  
Qy 856 TCCCGCGTGGACTACGGCAGCAGTCCGGGTCTGGTCTCAGGACACAGTGAAGGGGAAG 915  
Db 420 TCCCGCGTGGACTACGGCAGCAGTCCGGGTCTGGTCTCAGGACACAGTGAAGGGGAAG 361  
Qy 916 TTTGATGTCCAGTGGATTTTGTAAAGGATGTACCCATAACACAGCTCCCGGCACATCAGG 975  
Db 360 TTTGATGTCCAGTGGATTTTGTAAAGGATGTACCCATAACACAGCTCCCGGCATCAGG 301  
Qy 976 CTGAGAAATACGACAAACACCGGTACAAACTCCCGGGACACCCAGGAGGTGCCCTTA 1035  
Db 300 CTGAGAAATACGACAAACACCGGTACAAACTCCCGGGACACCCAGGAGGTGCCCTTA 241  
Qy 1036 GAAAAGCCAGCAAGTGTCTCAAAATTTATCAGTTCTTACAGGACACACACCTCCATCTTC 1095  
Db 240 GAAAAGCCAGCAAGTGTCTCAAAATTTATCAGTTCTTACAGGACACACACCTCCATCTTC 181  
Qy 1096 GACGACTTTGCTCACTACGAGAGCGCCA - GAGGAGGAGGAGGTGGTGGCGCAAGAAACGG 1154  
Db 180 GACGACTTTGCTCACTACGAGAGCGCCAGGAGGAGGAGGTGGTGGCGCAAGAAACGG 121  
Qy 1155 CAGAGTGGAAACAAATAGGGGGAACCAAGTTTCTTACATGTCTTAAACGTTTGACTTT 1214  
Db 120 CAGAGTGGAAACAAATAGGGGGAACCAAGTTTCTTACATGTCTTAAACGTTTGACTTT 61  
Qy 1215 GAAAACAGTTTTAAACAGTGTCTTGGTCAAGTCCAGTGTGGTCCCGTGGCGGGGTT 1274  
Db 60 GAAAACAGTTTTAAACAGTGTCTTGGTCAAGTCCAGTGTGGTCCCGTGGCGGGGTT 1

RESULT 16

BE892829 808 bp mRNA linear EST 20-OCT-2000  
LOCUS 60133961F1 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:391919 5',  
DEFINITION mRNA sequence.

ACCESSION

BE892829.1 GI:103533393

VERSION

EST.

KEYWORDS

human.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 808)  
NIH-MGC http://mgs.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DRP  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9748 row: i column: 16  
High quality sequence stop: 648.

FEATURES

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1. .808  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3919191"  
/clone\_lib="NIH\_MGC\_72"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Sali; skin; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: Sali; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2 kb. Library constructed by Life  
Technologies."  
222 a 172 c 163 g 251 t

BASE COUNT

222 a 172 c 163 g 251 t

ORIGIN

Query Match 28.7%; Score 581.8; DB 12; Length 808;  
Best Local Similarity 88.8%; Pred. No. 2e-114;  
Matches 711; Conservative 0; Mismatches 77; Indels 13; Gaps 7;  
Qy 977 TGGAGATAACGACAAACAAACCGGTACAAACTCCCGGACACCCAGGAGTGCCTTAG 1036  
Db 10 TGGAGATAACGACAAACAAACCGGTACAAACTCCCGGACACCCAGGAGTGCCTTAG 69  
Qy 1037 AAAAGCCAGCAGTGTCTGAAATTTATCAGTTCTTACAGCAGCAGCAGTCCATCTTCG 1096  
Db 70 AAAAGCCAGCAGTGTCTGAAATTTATCAGTTCTTACAGCAGCAGCAGTCCATCTTCG 129  
Qy 1097 ACGACTTTGCTCACTACGAGAGCGCCA - GAGGAGGAGGAGGTGGTGGCGAAGAACGGC 1155  
Db 130 ACGACTTTGCTCACTACGAGAGCGCCAGGAGGAGGAGGTGGTGGCGAAGAACGGC 189  
Qy 1156 AGAGTCGAAACAAACAAATAGGGCGAACCCAGTTTCTTACATGTTCCTAACGTTGACTTTG 1215  
Db 190 AGAGTCGAAACAAACAAATAGGGCGAACCCAGTTTCTTACATGTTCCTAACGTTGACTTTG 249  
Qy 1216 AAAACAGTTTTAAACACAGTGTGTGGTGTGCTCAGTCCAGTGTGTGCTCCGTCGGGGGTTG 1275  
Db 250 AAAACAGTTTTAAACACAGTGTGTGGTGTGCTCAGTCCAGTGTGTGCTCCGTCGGGGGTTG 309  
Qy 1276 AGTGTTCATCTTTTGGCCTTTCTTGTGCTGATTTTTTCCCGCAGATGGATCTGCAATTTATTT 1335  
Db 310 AGTGTTCATCTTTTGGCCTTTCTTGTGCTGATTTTTTCCCGCAGATGGATCTGCAATTTATTT 369  
Qy 1336 GTACTTTTTCTATGTATATAATCCCTGTAGAGTCACTAATAAGGAGTATTTTTTTTTT 1395  
Db 370 GTACTTTTTCTATGTATATAATCCCTGTAGAGTCACTAATAAGGAGTATTTTTTTTTT 428  
Qy 1396 TCAGCTTTATCAATCAGACTGATCTAATGTGAAATGTAAAGTATCCTTTAAACAAAGCATC 1455  
Db 429 TCAGCTTTATCAATCAGACTGATCTAATGTGAAATGTAAAGTATCCTTTAAACAAAGCATC 489





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QY 1318 ATGGATCTGCATTATTTTGTACTTTTCTTATGAT 1352
Db 42 ATGGATCTGCATTATTTTGTAAATCTCGGATGAT 8

RESULT 20
BG249197
DEFINITION
602361623F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4470316 5',
mRNA sequence.
ACCESSION
BG249197
VERSION
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 929)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs@mail.nih.gov
Tissue Procurement: ARCC
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10287 row: m column: 05
High quality sequence stop: 629.

FEATURES
source
1..929
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4470316"
/clone_lib="NIH MGC 89"
/tissue_type="hypernephroma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: Kidney; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
BASE COUNT 191 a 205 c 207 g 326 t
ORIGIN

Query Match 27.3%; Score 553.4; DB 12; Length 929;
Best Local Similarity 92.0%; Pred. No. 2.5e-108;
Matches 674; Conservative 0; Mismatches 46; Indels 13; Gaps 8;

QY 1217 AACAGTTTAAACACGTGTGCTTGGTCAGCTCCAGTGTGTCGCCGTGGGGGTGA 1276
Db 13 AACAGTTTAAACACGTGTGCTTGGTCAGCTCCAGTGTGTCGCCGTGGGGGTGA 72
QY 1277 GTGTGATCTTCCCTTCTTGTGCTGATTTTGGCCAGATGATCTGCATTATTG 1336
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QY 1337 TACTTTTCTATGATATATACTCTGTAGAGTCACTAATAAAGAGTATTTTTTGT 1396
Db 133 TACTTTTCTATGATATATACTCTGTAGAGTCACTAATAAAGAGTATTTTTTGT 191
QY 1397 CAGCTTATCAATCAGATGATCTAATGTGAATGAAGTATCTTTAAACAAAGCATCT 1456
Db 192 CAGCTTATCAATCAGATGATCTAATGTGAATGAAGTATCTTTAAACAAAGCATCT 251
QY 1457 ATTTTGGCAGAAATGTGTTCTTAATTCAGTCACTTTGATATCTGTGAGACTTCATAT 1516
Db 252 ATTTTGGCAGAAATGTGTTCTTAATTCAGTCACTTTGATATCTGTGAGACTTCATAT 311
QY 1517 TCTCATCCCTTTATTTGCTTTTATAGCAACATAAGAAACCATGAGTCACTTTGTCAATTAG 1576

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Db 312 TCTCATCCCTTTATTTGCTTTTGTAGCAAAACATAAGAAACCATGATCA-TTGTGCAATTAG 370
QY 1577 AGTATTTCTGATAAAATCTCTTGAAATATCTGAAATCAAAAGGTTAATGATTTTGTTC 1636
Db 371 AGTATTTCTGATAAAATCTCTTGAAATATCTGAAATCAAAAGGTTAATGA-TTTTGTTC 429
QY 1637 TTCTGATTTGTCATTTTATTAATCTGTTATCGGTCTAAAGTGTCTAAATTTACCCATTGAT 1696
Db 430 TTCTGA-TTGTCACTTTTATTAATCTGTTATCGGTCTAAAGTGTCTAAATTTACCCATTGAT 488
QY 1697 TTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGCACACACTTTTTCATTTT 1756
Db 489 TTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGCACACACTTTTTCATTTT 548
QY 1757 T-GAAATCTTTCTTCCAGATCTGTGCCCCTGAAACAGCCACCGTCCCTCACTGTCC 1815
Db 549 TCGAAATCTTTCTTCCAGATCTGTGCCCCTGAAACAGCCACCGTCCCTCACTGTCC 608
QY 1816 TGTGTCCGATTTGGGCTGAT-GGTGTGGGCATGATGTGGAGGAAGTGGAGGTGC 1874
Db 609 TGTGTCCGATTTGGGCTGATGTGGGTGTCGGGGCATGATGTGTGGCGGA--CTGCAGGTGC 666
QY 1875 TTAGGTCTGTTTCAGGTCGGGCATTTCTTTGTTTGCACATCTTTTAAATTTTACA 1934
Db 667 TTAGGTCTGTTTCAGGTCGGGCATTTCTTTGTTTGCACATCTTTTAAATTTTACA 721
QY 1935 CCTTTTCTTAAAGA 1947
Db 722 CCTTTTCTTAAAGA 734

RESULT 21
AW387761/c
LOCUS
MR4-ST0118-041099-010-C01 ST0118 Homo sapiens cDNA, mRNA sequence.
DEFINITION
AW387761
ACCESSION
AW387761.1 GI:6892420
VERSION
EST.
KEYWORDS
human.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 563)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=RC0&t2=MR4-ST0118-
041099-010-C01&t3=1999-10-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 523.
Location/Qualifiers
1..563
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0118"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under

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low stringency conditions."  
BASE COUNT 116 a 161 c 139 g 147 t

Query Match 27.2%; Score 551; DB 10; Length 563;  
Best Local Similarity 99.8%; Pred. No. 8.4e-108; Mismatches 0; Indels 1; Gaps 1;  
Matches 562; Conservative 0;

QY 713 TTAAGTACTCCATCTGGTGTAGCAGACGCGCAACAGCGCTGACAGCGCCCTTCC 772  
DB 563 TTAAGTACTCCATCTGGTGTAGCAGACGCGCAACAGCGCTGACAGCGCCCTTCC 504  
QY 773 GCTGCATGAGCAGCAGAGGGGCGCTTACCTGCTTTCAGCGTCAATGGGAGTGGGCAAT 832  
DB 503 GCTGCATGAGCAGCAGAGGGGCGCTTACCTGCTTTCAGCGTCAATGGGAGTGGGCAAT 444  
QY 833 TTTCTGGGTCGCGCAGATGAAGTCCCGCTGGACTACGGCACCGATGCGGGGTCTGGT 892  
DB 443 TTTCTGGGTCGCGCAGATGAAGTCCCGCTGGACTACGGCACCGATGCGGGGTCTGGT 384  
QY 893 CTCAGGCAAGTGGAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGGATGTACCCA 952  
DB 383 CTCAGGCAAGTGGAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGGATGTACCCA 324  
QY 953 ATACCAGCTCCGCGACATCAGGCTGGAGATAGGACAAACACCGGTACAAACTCCC 1012  
DB 323 ATACCAGCTCCGCGACATCAGGCTGGAGATAGGACAAACACCGGTACAAACTCCC 264  
QY 1013 GGGACACCCAGAGGTGCCCTTAGAAAAGCAAGCAAGTCTGAAAATTATCATGTTCT 1072  
DB 263 GGGACACCCAGAGGTGCCCTTAGAAAAGCAAGCAAGTCTGAAAATTATCATGTTCT 204  
QY 1073 ACAAGCACACACCTCCATCTTCAGCAGCTTTGCTCACTACGAGAAGGCCA-GAGGAGG 1131  
DB 203 ACAAGCACACACCTCCATCTTCAGCAGCTTTGCTCACTACGAGAAGGCCAAGGAGG 144  
QY 1132 AGGAGTGTGCGCAGAGGAGCGGAGTCCAAACAAATAGGCGGAACCACTTCT 1191  
DB 143 AGGAGTGTGCGCAGAGGAGCGGAGTCCAAACAAATAGGCGGAACCACTTCT 84  
QY 1192 TACATGTTCTAAAGTTTGACTTTGAAAACAGTTTAAACACAGTGTGCTGAGCTCCA 1251  
DB 83 TACATGTTCTAAAGTTTGACTTTGAAAACAGTTTAAACACAGTGTGCTGAGCTCCA 24  
QY 1252 GTGTGCTGCTCCCGTGGGGGGT 1274  
DB 23 GTGTGCTGCTCCCGTGGGGGGT 1

RESULT 22  
BG216572  
LOCUS BG216572  
DEFINITION RST36264 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
ACCESSION BG216572  
VERSION BG216572.1 GI:13742593  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,  
Lerner, L., Costanzo, D., McElligott, K., Booser, S., Maya, R., Smith,  
E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher,  
J.J., Danzig, J. and Ducar, M.  
Creation of genome-wide protein expression libraries using random  
activation of gene expression  
Nat. Biotechnol. 19 (5), 440-445 (2001)  
2127151  
Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@athersys.com  
High quality sequence stop: 377.  
Location/Qualifiers

source

1. .893  
/organism="Homo sapiens"  
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/clone\_lib="Athersys RAGE Library"  
/cell\_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 247 a 195 c 147 g 303 t  
ORIGIN

Query Match 26.9%; Score 545.6; DB 12; Length 893;  
Best Local Similarity 89.9%; Pred. No. 1.2e-106;  
Matches 607; Conservative 0; Mismatches 65; Indels 3; Gaps 2;

QY 1146 AAGAACGGCAGAGTCGAAACAACATGAGGGGACCACTTCTTACATGTTCTAACG 1205  
DB 4 ATGGAACACAGAGTCGAACTTCAATGAGGACCACTTCTTACATGTTCTAACG 63  
QY 1206 TTTGACATTTGAAACACAGTTTAAACACAGTGTGTTGTCAGCTCCAGTGTGTCGCCGT 1265  
DB 64 TTTGACATTTTAAACACAGTTTAAACACAGTGTGTTGTCAGCTCCAGTGTGTCGCCGT 123  
QY 1266 GCGGGGTTCAGTGTTCGATCTTTGCGCTTTGCTGCTGATTTTTCGCCAGATGGATCT 1325  
DB 124 GCGGGGTTCAGTGTTCGATCTTTGCGCTTTGCTGCTGATTTTTCGCCAGATGGATCT 183  
QY 1326 GCATTTATTTGTAATTTCTATGATTAATCTCTAGAGTCATTAATAGAGGAGTA 1385  
DB 184 GCATTTATTTGTAATTTCTATGATTAATCTCTAGAGTCATTTTAAAGGAGTA 243  
QY 1386 TTTTTCCTGTCAGCTTATCAATCAGACTGATCTAATGTGAAATGTAAATTCCTTAAAA 1445  
DB 244 -TTTTCCTGTCAGCTTATCAATCAGACTGATCTAATGTGAAATGTAAATTCCTTAAAA 302  
QY 1446 ACAAGCATCTATTTGGCAGAAATTTGTTCTTAAATTCAGTCAATTTGATTCGTGA 1505  
DB 303 ACAAGCATCTATTTGGCAGAAATTTGTTCTTAAATTCAGTCAATTTGATTCGTGA 362  
QY 1506 GACTTCATATTTCTCATCCCTTTATTCGCTTTTAGCAACATAGAACCATGAGTCATT 1565  
DB 363 GACTTCATATTTCTCATCCCTTTATTCGCTTTTAGCAACATAGAACCATGAGTCATT 422  
QY 1566 TTGTCAATTTAGAGTATTTCTGATAAAATCTCTTGAAAAATCTGAAATCAAAAGGTTAATGA 1625  
DB 423 TTGTCAATTTAGAGTATTTCTGATAAAATCTCTTGAAAAATCTGAAATCAAAAGGTTAATGA 482  
QY 1626 TTTTTCCTGTCATTCGTATTTGTCATTTATTAATTCGTATTCGGTCTAAAGTCTAATTTA 1685  
DB 483 TTTTCCTGTCATTCGTATTTGTCATTTAATATTCGTCTCGTCTAAAGTCTAATTTA 542  
QY 1686 CCCATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAATTTTGCAGACACTTT 1745  
DB 543 CCCATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTGTGAAATTCGGCACACTCTCT 602  
QY 1746 TTTTTCCTGTCATTTGAAAAATCTTTCTTCAGATCTGTTGCCACTGAAACAGCCCGCTCC 1805  
DB 503 TTTTTCCTGTCATTTGAAAAATCTTTCTTCAGATCTGTTGCCACTGAAACAGCCCGCTCC 660  
QY 1806 CTCACCTGCTGGTG 1820  
DB 661 CTCACCTGCTGGTG 675

RESULT 23

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BM014798      688 bp      mRNA      linear      EST 30-OCT-2001
LOCUS      603640668F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5416745 5',
DEFINITION      mRNA sequence.
ACCESSION      BM014798
VERSION      BM014798.1 GI:16529152
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 688)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12063 row: g column: 18
High quality sequence stop: 679.
FEATURES             Location/Qualifiers
     source          1..688
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NIH_MGC_87"
                     /tissue_type="mammary adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: breast; Vector: pCMV-SPORT6; Site: 1: NotI;
                     Site: 2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.383 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH MGC Library."
BASE COUNT      174 a 118 c 140 g 256 t
ORIGIN
Query Match      26.8%; Score 542.8; DB 13; Length 688;
Best Local Similarity 94.8%; Pred. No. 4.7e-106;
Matches 626; Conservative 0; Mismatches 27; Indels 7; Gaps 6;

QY 1374 AATAAGGAGTATTTTGTGCGCTATCAATCAGCTGATCTAATGTGAATCTAA 1433
DB 1 AATAAGGAGTA-TTTTTTGTGCGCTATCAATCAGCTGATCTAATGTGAATCTAA 59

QY 1434 GTATCCTTAAAAACAAGCATCTATTTGGCAGAAATGTGTTCTTAAATTCAGTCAATT 1493
DB 60 GTATCCTTAAAAACAAGCATCTATTTGGCAGAAATGTG-TCTTAAATTCAGTCAATT 118

QY 1494 GATATTCGTGAGACTCATATTTCTCATCCCTTATGCTTTTGTAGCAACATAAGAAA 1553
DB 119 GATATTCGTGAGACTCATATTTCTCATCCCTTATGCTTTTGTAGCAACATAAGAAA 178

QY 1554 CCATGAGTCATTTGTCTATTTAGAGTATCTGATAAATCTCTGAAATCTGAATCA 1613
DB 179 CCATGAGTCATTTGTCTATTTAGAGTATCTGATAAATCTCTGAAATCTGAATCA 238

QY 1614 AAAGTTAATCATTTTGTTCATTCGTATTTGTCATTTTATATCTGTTATCGGCTCAA 1673
DB 239 AAAGTTAATCATTTTGTTCATTCGTATTTGTCATTTTATATCTGTTATCGGCTCAA 298

QY 1674 AGTGCTAATTTACCCTATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTT 1733
DB 299 AGTGCTAATTTACCCTATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTT 358

QY 1734 GGCAGACACTTTTTTTTTT-TTTTGGAAATCTTTTCCCTTCAGATCTGTGTGCCCACTGAA 1792
DB 359 GGCAGACACTTTTTTTTTTCTTTGGAAATCTTTTCCCTTCAGATCTGTGTGCCCACTGAA 418
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QY 1793 CAGCCACCCGCTCCCTCCTCCTGCTGTCCTGATGGGCTGGATGCTGTGGGCGCATGAT 1852
DB 419 CAGCCACCCGCTCCCTCCTCCTGCTGTCCTGATGGGCTGGATGCTGTGGGCGCATGAT 478

QY 1853 GTGTGGAGGAACCTGGAAGTGCTTTTAGGTCCTGTTTCAGGCTCGGGCATCTTTTGTG--T 1910
DB 479 GTGTGGAGGACACTGGAAGTGCTTAGGTCCTGTTTCAGGCTCGGGCATCTTTTGTGTC 538

QY 1911 TTGCACATCTTTTAAATTTTACACCTTTTCTTAAGAAATCTTAATCCCGTCTTAAGTTTT 1970
DB 539 TTGCACATCTTTTGAATTTTACACCTTTTCTTAAGAAATCTTAATCCCGTCTTAAGTTTT 598

QY 1971 TATACCAATAAGTCTGAGCTTTAAG-TGTAGAT-CTGTAGTACAGACAGTGTGATGGA 2028
DB 599 TATCCCAATAATGCTGAGCTTTAAGCTGTAGGATCCGGGTAGTACAGACAGTGTGATGGA 658

RESULT 24
BE542593      837 bp      mRNA      linear      EST 09-AUG-2000
LOCUS      601063983F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450261 5',
DEFINITION      mRNA sequence.
ACCESSION      BE542593
VERSION      BE542593.1 GI:9771238
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 837)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8428 row: f column: 22
High quality sequence stop: 631.
FEATURES             Location/Qualifiers
     source          1..837
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NIH_MGC_10"
                     /cell_line="MGC36"
                     /lab_host="DH10B"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1: NotI;
                     Site: 2: SalI; Cloned unidirectionally. Primer: oligo dT.
                     Average insert size 1.5 kb. Library prepared by Life
                     Technologies."
BASE COUNT      193 a 231 c 252 g 161 t
ORIGIN
Query Match      25.6%; Score 519.2; DB 10; Length 837;
Best Local Similarity 92.8%; Pred. No. 5.3e-101;
Matches 655; Conservative 0; Mismatches 38; Indels 13; Gaps 10;

QY 577 AGGCTCGAATCCCAACCCCGCTCTTGAATAACTGAAGCTGCTCACAGCTACACCCGAAA 636
DB 1 AGGCTCGAATCCCAACCCCGCTCTTGAATAACTGAAGCTGCTCACAGCTACACCCGAAA 60

QY 637 GAGTTTTCAGTGGAAATCTGAAAGCGGCGGTGTTCAT-CATCAAGAGTACTCTTGAGGA 695
DB 61 GAG-TTCAGTGGAAATCTGAAAGCGGCGGTGTTCATCCATCAAGAGTACTCTTGAGGA 119

QY 696 CGACATCCACCG-CTCCATTTAAGTACTCCATCTGTTGTAGACAGACGCGCAACAGC 754
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Db 120 CGACATCCACCGCTCCATTAAGTACTCATCTGCTAGCAGACGACGCAACAGC 179
Qy 755 GCCTGGACAGCGCTTCGCCGCGCATGAGCAGCAAGGCGCGCTTACTGCTCTTACG 813
Db 180 GCCTGGACAGCGCTTCGCCGCGCATGAGCAGCAAGGCGCGCTTACTGCTCTTACG 239
Qy 814 GTCATAGGAGTGCGCATTTTGTGGGTGCGCGAGATGAAGTCCCGTGGACTACGCG 873
Db 240 GTCATAGGAGTGCGCATTTTGTGGGTGCGCGAGATGAAGTCCCGTGGACTACGCG 297
Qy 874 ACCAGTCCCGGCTGCTGCTCAGACACAGTGGAGGGAAGTTGATGTCAGTGGATT 933
Db 298 ACCAGTCCCGGCTGCTGCTCAGACACAGTGGAGGGAAGTTGATGTCAGTGGGA-T 356
Qy 934 TTTGTTAAGGATGTACCAATAACAGCTCCGGGACATCAGCTGGAGAAATACGACAA 993
Db 357 TTTGTTAAGGATGTACCAATAACAGCTCCGGGACATCAGCTGGAGAAATACGACAA 416
Qy 994 AAACCGGTCAAAACTCCCGGACACCCAGGAGTGCGCTTTAGAAAAGCCCAAGTG 1053
Db 417 AAACCGGTCAAAACTCCCGGACACCCAGGAGTGCGCTTTAGAAAAGCCCAAGTG 476
Qy 1054 CTGAATATATCAGTCTCTACAGCACACACCTCCATCTTCGACGACTTTGCTCAGTAC 1113
Db 477 CTGAATATATCAGTCTCTACAGCACACACCTCCATCTTCGACGACTTTGCTCAGTAC 536
Qy 1114 GAGAAGGCCAG--AGGAGGAGGAGTGCGGCAAGGAGGAGTGCGGCAAGGAGTGCGGCA 1171
Db 537 GAGAAGGCCAGGAGGAGGAGGAGTGCGGCAAGGAGGAGTGCGGCAAGGAGTGCGGCA 595
Qy 1172 ATGAGGCGCAACAGTCTTCTACATGTTCTAAGTCTTCTAAGTCTTCTAAGTCTTCTA 1231
Db 596 AATGGGGGAACAGTCTTCTACATGTTCTAAGTCTTCTAAGTCTTCTAAGTCTTCTA 652
Qy 1232 CGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1277
Db 653 CGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 698

RESULT 25
AL562740/c 921 bp mRNA linear EST 16-FEB-2001
LOCUS AL562740 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC020Y104 3
DEFINITION prime, mRNA sequence.
ACCESSION AL562740
VERSION AL562740.1 GI:12911458
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1. 921
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="CS0DC020Y104"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_types="neuroblastoma cells"
/lab_hosts="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
```

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vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com*
BASE COUNT 323 a 196 c 170 g 222 t 10 others
ORIGIN
Query Match 25.6% Score 519; DB 9; Length 921;
Best Local Similarity 98.5% Pred No. 5.8e-101;
Matches 517; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
Qy 1504 GAGACTTTCATATTTCTCATCCCTTTATTGCTTTTGTAGCAACATAAGAAACCATGAGTCA 1563
Db 921 GAGACTTTCATATTTCTCATCCCTTTATTGCTTTTGTAGCAACATAAGAAACCATGAGTCA 862
Qy 1564 TTTTGTCTATTAGAGTATTCGTATAAAATCTCTTGAATAATCTGAAATCTGAAAGGTTAAT 1623
Db 861 TTTTGTCTATTAGAGTATTCGTATAAAATCTCTTGAATAATCTGAAATCTGAAAGGTTAAT 802
Qy 1624 GATTTTGTGTTTCTATCTGATTTGTCATTTTATTTATCTGTTATCGTCTGAAAGTCTAAT 1683
Db 801 GATTTTGTGTTTCTATCTGATTTGTCATTTTATTTATCTGTTATCGTCTGAAAGTCTAAT 742
Qy 1684 TACCATTTGATTTTCTGCTAGACAGATAAATCTTTTAAATTTTTCAGAGACACT 1743
Db 741 TACCATTTGATTTTCTGCTAGACAGATAAATCTTTTAAATTTTTCAGAGACACT 682
Qy 1744 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1803
Db 681 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 622
Qy 1804 CCCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1863
Db 621 CCCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 562
Qy 1864 CTGGAAGGTGCTTTTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1923
Db 561 CTGGAAGGTGCTTTTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 502
Qy 1924 TAAATTTTACACCTTTTCTTAAAGAAATCTAATGCGCTTAAAGTCTTAAAGTCTTAAAGT 1983
Db 501 TAAATTTTACACCTTTTCTTAAAGAAATCTAATGCGCTTAAAGTCTTAAAGTCTTAAAGT 442
Qy 1984 CTGAGCTTTAAGTGTAGGATCTGCTAGTACAGACAGTGTGATGGA 2028
Db 441 CTGAGCTTTAAGTGTAGGATCTGCTAGTACAGACAGTGTGATGGA 397

RESULT 26
BM931439 598 bp mRNA linear EST 13-MAR-2002
LOCUS BM931439
DEFINITION UI-E-EJ1-ajg-a-05-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone
UI-E-EJ1-ajg-a-05-0-UI 5', mRNA sequence.
ACCESSION BM931439
VERSION BM931439.1 GI:19390612
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 598)
JOURNAL Bonaldo, M.F., Lennon, G. and Soares, M.B.
COMMENT Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
```





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Qy 835 TGTGGGTGGCGAGATGAAGTCCCTCCCTGGAGTACGCACAGTCCCGGGTCTGGTCT 894
Db 242 TGTGGGTGGCGAGATGAAGTCCCTCCCTGGAGTACGCACAGTCCCGGGTCTGGTCT 301
Qy 895 CAGCACAAGTGGAGGGGAAGTTTATGATCCAGTGGATT--TTGTTAAGGATGTACCCA 952
Db 302 CAGCACAAGTGGAGGGGAAGTCTGATGTCAGTGGATT--TTGTTAAGGATGTACCCA 361
Qy 953 ATAACCAAGTCCCGCACATCAGGCTGGAGAAATAGCACAACAAACCGGTACAAACTCCC 1012
Db 362 ATAACCAAGTCCCGCACATCAGGCTGGAGAAATAGCACAACAAACCGGTACAAACTCCC 421
Qy 1013 GGGACACCCAGAGGTGCCCTTAG--AAAAAGCCCAAGTGTCTGAAATTTATCAGTTC 1070
Db 422 GGGACACCCAGAGGTGCCCTTAGCACAACAAAGCCCAAGTGTCTGAAATTTATCAGTTC 481
Qy 1071 CTACAGCACAACCTCCATCTTCGAGACTTTCCTCACTACGAGAGCCCA-GAGGA 1129
Db 482 CTACAGCACAACCTCCATCTTCGAGACTTTCCTCACTACGAGAGCCCAAGGAGGA 541
Qy 1130 GGAGAGGTGGTG-CGCAAGGAACGGCAGAGTCCGAACAACAATGA 1175
Db 542 GGAGAGGTGGTGCGCGAAGGAACGGCGCAGCTCGCACAACCCAGA 588

RESULT 28
AW387819 659 bp mRNA linear EST 04-FEB-2000
LOCUS MR4-ST0118-021299-021-a06 ST0118 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW387819
ACCESSION AW387819.1 GI:6892478
VERSION EST.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 659)
AUTHORS HCSP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4st2=MR4-ST0118-
021299-021-a06&tl=1999-12-02&tl=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 658.
FEATURES
source 1..659
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0118"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 178 a 175 c 179 g 127 t
ORIGIN

```

Query Match

24.8%; Score 503.6; DB 10; Length 659;

Best Local Similarity 95.8%; Pred. No. 1.2e-97;  
Matches 571; Conservative 0; Mismatches 19; Indels 6; Gaps 5;

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Qy 559 CAGCTTAATTTCTGCCCCCAGCGTCGAATCCACCCCGCTCTTGAATAAATCGAAGCGTCT 618
Db 22 CAGCTTAATTTCTG--CCAGCGTCGAATCCACCCCGCTCTTGAATAAATCGAAGCGTCT 79
Qy 619 CACAGCTACAAACCCGAAAGAGTTTGAAGTGGAAATCTGAAAAA-GCGGGGGTGTGTTTCATCAT 677
Db 80 ACGAGCTACAAACCCGAAAGAGTTTGAATGGAATCTGAAAAAGCGGGCGTGTGTTTCATCAT 139
Qy 678 CAA-GAGCTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCTCATCTGGTGTAGCA 736
Db 140 CAATGAGCTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCTCATCTGGTGTAGCA 199
Qy 737 CAGAGCACGGCAACAACGCGCTGGACAGCGCTTCCCTGTCATGAGCAGCAAGGGGGCCG 796
Db 200 CAGAGCACGGCAACAACGCGCTGGACAGCGCTTCCCTGTCATGAGCAGCAAGGGGGCCG 259
Qy 797 TCTACCTGCTCTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGGTGGCCGAGATGAAGT 856
Db 260 TCTACCTGCTCTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGGTGGCCGAGATGAAGT 319
Qy 857 CCCCCTGGACTACGGCACCAAGTCCC--GGGCTCTGGTCTCAGGACAAGTGGAAAGGGAAG 915
Db 320 CCCCCTGGACTACGGCACCAAGTCCC--GGGCTCTGGTCTCAGGACAAGTGGAAAGGGAAG 379
Qy 916 TTTGATCTCCAGTGGATTTTGTAAAGATGTATCCC--AATAACCCAGCTCCGGCACATCAG 974
Db 380 TTTGATCTCCAGTGGATTTTGTAAAGATGTATCCC--AATAACCCAGCTCCGGCACATCAG 439
Qy 975 GCTGGAGATAACGACAACAACCCGGTCAACAACCTCCCGGGACACCCAGGAGTGGCCCTT 1034
Db 440 GCTGGAGATAACGACAACAACCCGGTCAACAACCTCCCGGGACACCCAGGAGTGGCCCTT 499
Qy 1035 AGAAAAAGCCAAAGCAAGTGTCTGAAAAATTTATCAGTTCCTACAAGCACAACAACCTCCTT 1094
Db 500 AGAAAAAGCCAAAGCAAGTGTCTGAAAAATTTATCAGTTCCTACAAGCACAACAACCTCCTT 559
Qy 1095 CGACGACTTTGCTCCTACCTACGAGAGCGCCAGAGGAGGAGTGGTGGCCCAAGGA 1150
Db 560 CGACGACTTTGCTCCTACCTACGAGAGCGCCAGAGGAGGAGTGGTGGCCCAAGGA 615

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## RESULT 29

BF915645/c 530 bp mRNA linear EST 18-JAN-2001  
LOCUS IL3-UT0114-061200-373-C06 UT0114 Homo sapiens cDNA, mRNA sequence.

DEFINITION BF915645

ACCESSION BF915645

VERSION BF915645.1 GI:12307103

KEYWORDS EST.

SOURCE human.

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 530)

AUTHORS Nagai, M.A., da Silva, W. Jr., Zagor, M.A., Bordin, S., Costa, F.F.,

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

, M.J., Soares, F., Brentani, R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001



```
Qy 1195 ATGTTCTAACGTTGACATTTGAAACACAGTTTAAACACAGTGTGTGCTTGTCTAGCTCCAGTG 1254
|||||
Db 74 ATGTTCTAACGTTGACATTTGAAACACAGTTTAAACACAGTGTGTGCTTGTCTAGCTCCAGTG 15
|||||
Qy 1255 TGTGTCCTCCGTCGG 1268
|||||
Db 14 TGTGTCCTCCGTCGG 1

RESULT 31
AJ449334
LOCUS AJ449334 riken1 Gallus gallus cDNA clone 21k24r1, mRNA sequence. EST 19-APR-2002
DEFINITION AJ449334
ACCESSION AJ449334
VERSION AJ449334.1 GI:20216555
KEYWORDS EST.
SOURCE Chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 688)
Buerstedde, J.M.
Gallus gallus bursal lymphocyte EST
Unpublished (2002)
Contact: Buerstedde JM
Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20351 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
FEATURES
source
1. 688
/organism="Gallus gallus"
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/clone="21k24r1"
/clone_lib="riken1"
/cell_type="bursal lymphocyte"
/dev_stage="2-3 weeks old"
/notes="CB inbred strain"
BASE COUNT 206 a 156 c 157 g 169 t
ORIGIN
Query Match 23.8%; Score 483.6; DB 9; Length 688;
Best Local Similarity 82.5%; Pred. No. 2.3e-93;
Matches 566; Conservative 0; Mismatches 119; Indels 1; Gaps 1;

Qy 440 CGCAGTATCAGAGCCCTCAGCAGCCACCCAGACCCGCTGGTGGTGGCCCGCCAGCAGACAGAA 499
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Db 2 CACAGTATCAGAGCCCTCAGCAGCCACCCAGACCCGCTGGTGGTGGCCCGCCAGCAGACAGAA 61
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Qy 500 ACGCGGCTTTGGGCGAGCGAGGGGCTGGCAGCGATAGCAACTCTCTCGAAACGTC 559
|||||
Db 62 ATGAGCTTTTGGCGAAGTGGAGGAATGTAATGACAGCAATTCAGCTGGCAGTACCC 121
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Qy 560 AGCCTAAATCTGCCCGCCAGCGTGAATCCCAACCCCGCTCTTGAAGAACTGAAGCTGCTC 619
|||||
Db 122 AGCCTAACCCCTGTTCCAAGTGGTGGTCCCATCTCTGTTTGAAGAACTGAAGCTGCTC 181
|||||
Qy 620 ACAGCTAACCCGAAAGAGTTTGAAGTGAATCTGAAGCGGGCGGTGTGTTCATCATCA 679
|||||
Db 182 ACAGCTAATCTTAAAGATTTTGAATGGAACCTTAAAGATGACGTTGTGTTCATAATA 241
|||||
Qy 680 AGAGCTACTCTGAGACGACATCACCGCTCCATTAACTACTCCATCTGCTGTGTAGCAG 739
|||||
Db 242 AGAGCTATTCTGAGAGATGATATTATCGTTCCATTAACTATTCTATTGTTGTAGTACGG 301
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Qy 740 AGCAGGCAACAGCGCTTGACAGCGCTTCCGCTGCATGAGCAGCAAGGGGCCCGTCT 799
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Db 302 AGCATGGCAACAAACGCGCTGGACAGTGTCTTTTCGGTCCATGAATAGCAAGGCTCCGCT 361
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Qy 800 ACCTGCTCTTCAGCGTCATGGGAGTGGGCATTTTGTGGGGTGGCCGAGATGAAGTCCC 859
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Db 362 ACTTGCTATTCACTGTCAATGGCAGTGGACACTTCTCTGGAGTTGCAGAGATGAATCAC 421
Qy 860 CCGTGGACTAGCGCACCACTGCCGGGTCTGGTCTCAGGACAAGTGGAAAGGGAAATTTG 919
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Db 422 CTGTGGACTATGGCACCAGTGCAGTGTCTGGTCTCAGGACAAGTGGAAAGGGAAATTTG 481
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Qy 920 ATGTCCAGTGGATTTTGTAAAGATGTACCCAAATACCAAGTCCGGCAGACATCAGGCTGG 979
|||||
Db 482 ATGTCAAGTGGATCTTTGTGAAGGATGTGCCCAACCAACAGTCCGACACATCAGGCTGG 541
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Qy 980 AGAATAACGACACAAACCGGTCAAACT-CCGGGACACCCAGGAGGTGCCCTTAGAA 1038
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Db 542 AGACAATAGCAACAAACCTGTTACAAACTCCCGGTGACACACAGGAGGTGCCCTTAGAA 601
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Qy 1039 AAAGCCAAAGCAAGTGCAGAAATTTATCAGTTCTCTTACAAAGCACAACAACTTCATCTTGAC 1098
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Db 602 AAAGCAAAACAAGTGCATAAATTTATGCTACTTTACAAAGCACAACAACTTCATCTTTGAT 661
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Qy 1099 GACTTTGCTCACTACGAGAGCGCCA 1124
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Db 662 GACTTTTCTCATTTATGAAGAGCGCA 687
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RESULT 32
AW387916/c
LOCUS AW387916 499 bp mRNA linear EST 04-FEB-2000
DEFINITION MR4-ST0119-071099-010-F04 ST0119 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW387916
VERSION AW387916.1 GI:6892575
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 499)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-ST0119-
071099-010-F04&t3=1999-10-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 465.
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source
1. 499
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0119"
/dev_stage="Adult"
/notes="Organ: stomach; vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 103 a 144 c 118 g 134 t
ORIGIN
Query Match 23.7%; Score 480.6; DB 10; Length 499;
Best Local Similarity 99.0%; Pred. No. 1.1e-92;
Matches 494; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 777 CATGAGCAGCAAGGGGCCGCTCTACCTGCTCTTCAGCGCTCAATGGGAGTGGGCATTTTGG 836
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Db 499 CATGAGCAGCAAGGGCCCGCTACCTGCTCTTCAAGCTCAATGGAGTGGGCATTTTG 440
Qy 837 TGGGGTGGCCGAGTCAAGTCCCGCTGACTACGACAGTCCGGGTCTGGTCTCA 896
Db 439 TGGGGTGGCCGAGTCAAGTCCCGCTGACTACGACAGTCCGGGTCTGGTCTCA 380
Qy 897 GGAAGAAGTGAAGGGGAAGTTGATGCTCCAGTGGATTTTGTAAAGATGTACCCCAATAA 956
Db 379 GGACAAGTGAAGGGGAAGTTGATGCTCCAGTGGATTTTGTAAAGATGTACCCCAATAA 320
Qy 957 CAGCTCCGGCAGTCAAGTGGAGATACGACACAAACCGGTCAAACTCCCGGGA 1016
Db 319 CCAGCTCCAGCAGTCAAGTGGAGATACGACACAAACCGGTCAAACTCCCGGGA 260
Qy 1017 CACCCAGGAGTCCCTTAGAAAAAGCAAGCAAGTCTGAAAAATATCAGTTCCTACAA 1076
Db 259 CACCCAGGAGTCCCTTAGAAAAAGCAAGTCTGAAAAATATCAGTTCCTACAA 200
Qy 1077 GCACAACTCCATCTTCGACGACTTTGCTACTAGGAGAGCGCA-GAGGAGGAGGA 1135
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Qy 1136 GTGGTGGCAAGGAGCGGAGAGTGGAAACAAATGAGGGCGAACCAGTTCTTACA 1195
Db 139 GTGGTGGCAAGGAGCGGAGAGTGGAAACAAATGAGGGCGAACCAGTTCTTACA 80
Qy 1196 TGTTCTAACGTTTGACTTTGAAACAGTTTAAACACAGTCTGCTTGGTCAAGTCCAGTGT 1255
Db 79 TGTTCTAACGTTTGACTTTGAAACAGTTTAAACACAGTGTGAATGTCAGTCCAGTGT 20
Qy 1256 GTGCTCCCGTGGCGGGGTT 1274
Db 19 GTGCTCCCGTGGCGGGGTT 1

RESULT 33
LOCUS A0564196/c
DEFINITION HS 5363 A2 G07 T7A RPI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=939 Col=14 Row=M, DNA sequence.
ACCESSION A0564196
VERSION A0564196.1 GI:4923667
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 538)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 939 row: M column: 14
Seq primer: T7
Class: BAC ends
High quality sequence stop: 538.
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     /sex="male"
     /note="vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
BASE COUNT          210 a      95 c      92 g      138 t      3 others
ORIGIN
Query Match      23.7%; Score 480.4; DB 17; Length 538;
Best Local Similarity 97.2%; Pred. No. 1.2e-92;
Matches 487; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1439 CTTAAACAAAGCATCTATTTTGGCAGAAATGTGTTCTTAAATTCAGTCATTTGATAT 1498
Db 532 CTTAAACAAAGGCATCTATTTTGGCAGAAATGTGTTCTTAAATTCAGTCATTTGATAT 473
Qy 1499 TCTGTGAGACTTCATATTTCTCATCCCTTATTTAGCAACATAGAAACCATG 1558
Db 472 TCTGTGAGACTTCATATTTCTCATCCCTTATTTAGCAACATAGAAACCATG 413
Qy 1559 AGTCATTTTGTCAATTTAGAGTATCTGATAAAATCTTTGAAAAATCTGAAATCAAAAGG 1618
Db 412 AGTCATTTTGTCAATTTAGAGTATCTGATAAAATCTTTGAAAAATCTGAAATCAAAAGG 353
Qy 1619 TTAATGATTTTTTGTTCATTTCTGATTTGTCATTTTATTAATCTGTTATCGGTCTAAAGTGC 1678
Db 352 TTAATGATTTTTTGTTCATTTCTGATTTGTCATTTTATTAATCTGTTATCGGTCTAAAGTGC 293
Qy 1679 TAATTTACCATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAG 1738
Db 292 TAATTTACCATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAG 233
Qy 1739 ACATTTTTTTTTTTTTTGAATAATCTTTCCTTCCAGATCTGTTGCCACTGAACAGCCA 1798
Db 232 ACATTTTTTTTTTTTTTGAATAATCTTTCCTTCCAGATCTGTTGCCACTGAACAGCCA 173
Qy 1799 CCGCTCCCTCACTGCTCGTGTCCGATTTGGGCTGGATCGGTGTGGGGCATGATGTGTG 1858
Db 172 CCGCTCCCTCACTGCTCATGCTGCTGGATTTGGGCTGGATCGGTGTGGGGCATGATGTGTG 113
Qy 1859 AGGAATCGAAGTGTCTTTAGGTCTGGTTTCAGGTCGGGCATCTTTGTTGTTGGCAGAT 1918
Db 112 AGGAATCGAAGTGTGAAAAAGAGTCTGTTTCAGGTCGGGCATCTTTGTTGTTGGCAGAT 53
Qy 1919 CTTTTTAAATTTTACACCTTT 1939
Db 52 CTTTTAANNATTTACACCTTT 32

RESULT 34
LOCUS B1739961
DEFINITION B1739961 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5368251 5',
mRNA sequence.
ACCESSION B1739961
VERSION B1739961.1 GI:15716974
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 964)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
```

Email: csapbs-r@mail.nih.gov  
Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM1937 row: c column: 04  
High quality sequence stop: 754.  
Location/Qualifiers  
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/tissue\_type="retina"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."  
1 others  
BASE COUNT 283 a 199 c 247 g 234 t  
ORIGIN  
Query Match 23.5%; Score 476.4; DB 13; Length 964;  
Best Local Similarity 81.3%; Pred. No. 7.9e-92;  
Matches 645; Conservative 0; Mismatches 122; Indels 26; Gaps 7;  
Qy 673 ATCATCAAGAGCTACTCTGAGGAGGACATCCACCGCTCCATTAAGTACTCCATCTGGTGT 732  
Db 1 ATCATCAAGAGCTATTCTGAGGAGGACATCCACCGCTCCATCAAGTACTCCATCTGGTGT 60  
Qy 733 AGCAGAGAGCGGCAACAGCGCTGACAGCGCTTCCCTGCTGATGAGGAGGAGG 792  
Db 61 AGTACTGAACAGCGCAACAGCGCTGACAGCGCTTCCCTGCTGATGAGGAGGAGG 120  
Qy 793 CCCGCTACCTGCTCTTCAGCGTCAATCGGAGTGGGCAATTTTGTGGGTGGCGGAGATG 852  
Db 121 CCTGTTATCTCTCTTCAGTGTCAATGGGAGTGACATTTCTGTGGGTGGCGGAGATG 180  
Qy 853 AAGTCCCGGTGGAGTACGGACCAAGTCCCGGTGCTGGTCTCAGGACAAAGTGAAGGGG 912  
Db 181 AAGTCCCGGTGGAGTACGGACCAAGTCCCGGTGCTGGTCTCAGGACAAAGTGAAGGGG 240  
Qy 913 AAGTTGATGTCAGTGGATTTTGTGAAGATGTACCAATATACCAATACCAATCCCGGACATC 972  
Db 241 AAG-TTGAATGTAAGTGGATTTTGTGAAGATGTGCGCAACCAACCAAGCTCGCGCACATC 299  
Qy 973 AGGCTGGAGATTAACGACAAACCGGTCAAACTCCCGGGACACCCAGGAGTGCC 1032  
Db 300 AGACTGGAGATTAACGACAAACCGGTCAAACTCCCGGTGATACAGAGAGTGCC 359  
Qy 1033 TTAGAAAAAGCAAGCAAGTCTGAAATTAATCAAGTTCTTCAAGCAACACCACTCCATC 1092  
Db 360 TTAGAAAAAGCAAAACAGTCTGAAGATTATCGTTCTTATAGCAACACCACTCTATC 419  
Qy 1093 TTCACGACTTTGCTCACTACGAGAGCGCA-GAGGAGGAGGAGTGTGCGCAAGGAA 1151  
Db 420 TTTGACGACTTTTCTCATATTATGAGAGGCGCAGGAGGAGGAGTGTGCGTAAAGGAA 479  
Qy 1152 CGGAGAGTCCGAAACAAATAGGGGGAACCAAGTTCTTCTACATGTTCTAACGTTTGAC 1211  
Db 480 AGACAGATCGAAACAAACATATAGAACACCAAGTTGTTTGGT-----TATGTTGAC 535  
Qy 1212 TTTGAAAC--AGTTTAAACACGTGCTTGGTCAGTCTC-----CAGTGTGT 1257  
Db 536 TTTGAAACACAGATTTTAAAGCTGTATGCTTGGTGTCTCTCCGAGTCAAGTCCAGTGT 595  
Qy 1258 CGTCCGTCGGGGGTGAGTGTGTCATCTTTGCTTCTTGTGCTGATTTTGGCCAG 1317  
Db 596 CGTCCGTCGGGGGTGATTTGTCATCTTTATCTTTGTAG-----TTCAATTTTGGCCAG 651

Qy 1318 ATGATCTGCATTTATTTGTACTTTTCTATGTATTATAATCTCTGTAGACTCAATA 1377  
Db 652 ATGATCTGCATTTATTTGTATTTTCTATGTATTATAATCTCTGTAGACTCAATA 711  
Qy 1378 AAGAGATATTTTGTGTCAGCTTATCAATCAGACTGATCTAATGTGAATGTAAATAT 1437  
Db 712 AAGAGTA--TGGGCGCTCAGGTTATCAGTCAGCTTACCTAATGCAAAATATAAATAT 769  
Qy 1438 CCTTAAACAA 1450  
Db 770 TCTTCAAGAGAA 782  
RESULT 35  
BF529242  
LOCUS BF529242 937 bp mRNA linear EST 11-DEC-2000  
DEFINITION 602040117f1 NCI\_CGAP\_Brn67 Homo sapiens cDNA clone IMAGE:4177805  
5' mRNA sequence.  
ACCESSION BF529242  
VERSION BF529242.1 GI:11616605  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 937)  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: csapbs-r@mail.nih.gov  
Tissue Procurement: David N. Louis, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM9485 row: a column: 06  
High quality sequence stop: 634.  
Location/Qualifiers  
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/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."  
1 others  
BASE COUNT 242 a 183 c 214 g 297 t  
ORIGIN  
Query Match 23.4%; Score 475; DB 12; Length 937;  
Best Local Similarity 94.9%; Pred. No. 1.6e-91;  
Matches 577; Conservative 0; Mismatches 21; Indels 10; Gaps 8;  
Qy 1423 GTGAAATGTAAATCTCTTAAACAAAGCATCTATTTCGACAGAAATGTGTCTTAAA 1482  
Db 1 GTGAAATGTAAATCTCTTAAACAAAGCATCTATTTCGACAGAA--TGTGTCTTAAA 58  
Qy 1483 TTCAGTCATTGTATTTCTGTGAGCTTCATATTTCTCATCCCTTTATTTGCTTTTACGA 1542  
Db 59 TTCAGTCATTGTATTTCTGTGAGCTTCATATTTCTCATCCCTTTATTTGCTTTTACGA 118  
Qy 1543 AACATAGAACCATGAGTCAATTTGTTCATTAGAGTATTCTGATAAATCTCTTGA 1602  
Db 119 AACATAGAACCATGAGTCA--TTTGTCAATTAGATTTCTGTATAAATCTCTTGA 177

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QY 1603 TACTGAATCAAAAGGTTAATGATTTTTCATCTCTGATTTTGTCTATTTTATTATCTGT 1662
Db 178 TACTGAATCAAAAGGTTAATGATTTTTCATCTCTGATTTTGTCTATTTTATTATCTGT 236
QY 1663 TATCGGTCTAAAGTGCTAATTTTACCATTTGATTTTCTGCTAGACAGATACTTTTAAT 1722
Db 237 TATCGGTCTAAAGTGCTAATTTTACCATTTGATTTTCTGCTAGACAGATACTTTTAAT 296
QY 1723 TTTTCAAAATTTGCGAGACACTTTTTTTTTTTTTTTT-GAAAACTTTCTCCAGACTCTGT 1781
Db 297 TTTTCAAAATTTGCGAGACACTTTTTTTTTTTTTTTTGGAAAACTTTCTCCAGACTCTGT 356
QY 1782 TGCCCACTGAACAGCCACCGCTCCCTCA-CTGTCCTGGTGTCTCGATTTGGCTGGATGGTG 1840
Db 357 TGCCCACTGAACAGCCACCGCTCCCTCAATTGTCGGGTGTCCGATGGGGCTGGATGGTG 416
QY 1841 TTGGGGCATCATGTGTGAGGAACTGGAAGGTGCTTTAGGTCTGGTTTCAGGTCGGGCAT-1900
Db 417 TGGGGGCATCATGTGTGAGGAACTGGAAGGTGCTTTAGGTCTGGTTTCAGGTCGGGCAT 476
QY 1901 TCTTTGTTGTTTGCACACTTTTTTAAATTTTACACCTTTTCTTAAGAAATTTCTAATGCCGT 1960
Db 477 CCTTTGTTGTTTGCACACTTTTTTAAATTTTACACCTTTTCTTAAGAAATTTCTAATGCCG 533
QY 1961 CTTAAGTTTTTATACCAATTAATCTGAGCTTTAAGTGTAGATCTGCTAGTACAGACT 2020
Db 534 CTTAAGTTTTTATACCAATTAATCTGAGC-TTAAGTGTAGATCTGCTAGTACAGACCGT 592
QY 2021 GTGATGGA 2028
Db 593 GTGATGGA 600

RESULT 36
LOCUS BQ925658
DEFINITION AGENCOURT_8766458 NIH_MGC_130 Mus musculus cDNA clone IMAGE:632B298
5', mRNA sequence.
ACCESSION BQ925658
VERSION BQ925658.1 GI:22340689
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@f5000.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
Ph.D.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM13779 row: e column: 03
High quality sequence stop: 504.
Location/Qualifiers
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Site: EcorV, site 2: NotI; Cloned unidirectionally.
Primer: Oligo dr. Average insert size 1.95 kb.
constructed by ResGen, Invitrogen Corp. Note: this is a
NIH_MGC Library."
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BASE COUNT 281 a 232 c 230 g 259 t
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Query Match 23.3%; Score 472; DB 14; Length 1002;
Best Local Similarity 79.7%; Pred. No. 6.9e-91;
Matches 614; Conservative 0; Mismatches 135; Indels 21; Gaps 4;
QY 646 TGGATCTGAAAAGCGGGGTGTTCATCATCAAGAGTCTCTGAGGACGATCCAC 705
Db 10 TGGATCTTAAAGTGGGGGTGTTCATCATCAAGAGTCTCTGAGGACGATCCAC 69
QY 706 CGCTCCATTAAGTACTCTGCTAGCAGAGCAGCGCAACAGCGCCCTGGACGC 765
Db 70 CGCTCCATTAAGTACTCTGCTAGCAGAGCAGCGCAACAGCGCCCTGGACGC 129
QY 766 GCCTCCGCTGCTAGCAGAGCAGCGCGCCGCTTACCTCTCTTTCAGCGTCAATGGAGT 825
Db 130 GCCTCCGCTGCTAGCAGAGCAGCGCGCCGCTTACCTCTCTTTCAGTGTCAATGGAGT 189
QY 826 GGGCATTTTTTGGGGTGGCGGAGATGAAGTCCCCGTGGACTACGGCACCAGTCCGGG 885
Db 190 GGCATTTTCTGTGGGTGGCAGAGATGAAGTCCCCGTGGACTACGGCACCAGTCCGGG 249
QY 886 GTCTGCTCTCAGACAAAGTGGGAAAGTTTGTATGTCCAGTGAATTTTGTAAAGAT 945
Db 250 GTCTGCTCTCAGACAAAGTGGGAAAGTTTGTATGTCCAGTGAATTTTGTAAAGAT 309
QY 946 GTACCCATAAACCAGCTCCGGCACATCAGGCTGGGAAATAACGACAAACACCGGTCA 1005
Db 310 GTGCCCCAACACAGCTCCGGCACATCAGACTGGGAAATAACGACAAACACCGGTCA 369
QY 1006 AACTCCCGGACACCCAGAGGTGCCCTTAGAAAAAGCCAGCAAGTGTGAAAAATATC 1065
Db 370 AACTCCCGGTATACACAGAGGTGCCCTTAGAAAAAGCAAAACAGTGTGAAAGATTATC 429
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QY 1125 GAGGAGGAGGAGGTGGTGGCAAGGAAACGCGAGTTCGAAACAAACAAATGAGGCGCAAC 1184
Db 490 GAGGAGGAGGAGGTGGTGGCAAGGAAACGCGAGTTCGAAACAAACAAATGAGGCGCAAC 549
QY 1185 AGTTCTTACAGTTCTTAAGCTTTGACTTTGAAAAAGTCTGAAAAAGTCTGATCTGGTG 1241
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QY 1242 -----GTGAGTCCAGTGTGTCGTCCTGCGGGGGTTCGAGTGTGCACTTTTGC 1291
Db 610 CTGCTCCGAGTCCAGTCCCGGGGCAATCTCTGCGGGGGCTGATTTGTCATCTTAT 669
QY 1292 CTTTCTTGTGTTGATTTTGGCCAGATGGATCTGATTTTATTTGTACTTTT-----TCT 1346
Db 670 CTTTGGACTTCAT--TTTTCGCAATGGATCTGATTTTATTTCTGGATTTTCTATGG 727
QY 1347 ATGTATTATAATCTCTGAGAGTCACTAATAAGAGAGTATTTTTTTTGT 1396
Db 728 AATTATAAAATTTGTACAAACTCCCTAATAAAGGAGTATTTTTTGT 777

RESULT 37
LOCUS AW387858/c
DEFINITION MR4-ST0118-151299-023-b10 ST0118 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW387858
VERSION AW387858.1 GI:6892517
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 584)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
```



TITLE The FAPESP/LICR Human Cancer Genome Project  
JOURNAL Unpublished (1999)  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR4&st2=MR4-ST0118-  
151299-023-b10&t3=1999-12-15&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 496.

FEATURES  
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/db\_xref="taxon:9606"  
/clone\_lib="ST0118"  
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/notes="Organ: stomach; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
121 a 161 c 151 g 151 t

BASE COUNT 121 a 161 c 151 g 151 t  
ORIGIN  
Query Match 23.0%; Score 466.8; DB 10; Length 584;  
Best Local Similarity 92.9%; Pred. No. 9.5e-90;  
Matches 522; Conservative 0; Mismatches 37; Indels 3; Gaps 3;  
Qy 707 GCTCATTAACTACTCCATCTGGTGTAGCAGACGACGCGCAACAGCGCTCGACACGG 766  
Db 561 GCACCCCTCCATTAACTACTCTCTGGTGTAGCAGACGACGCGCTCGAAGCGC 502  
Qy 767 CTTTCGGTGTGATGAGCAGGAGGCGGCTACCTCTCTTCAGCGTCAATGGAGTG 826  
Db 501 CTTCCCTGGCATGAGCAGCAAGGCGGCTACCTCTCTTCAGCGTCAATGGAGTG 443  
Qy 827 GGCATTTTGTGGGTGGCGAGATGAAGTCCCGGTGGACTACGGCACCAGTCCCGGG 886  
Db 442 GGCATTTTGTGGGTGGCGAGATGAAGTCCCGGTGGACTACGGCACCAGTCCCGGG 383  
Qy 887 TCTGGTCTCAGGACAGTGGAGGGGAATTTGATGTCCAGTGGATTTTGTAAAGGATG 946  
Db 382 TCTGGTCTCAGGACAGTGGAGGGGAATTTGATGTCCAGTGGATTTTGTAAAGGATG 323  
Qy 947 TACCAATAACACCTCCGCGACATCAGCTGGAGATAACGACAAACACCGGTCAAA 1006  
Db 322 TACCCCATTAACAGCTCCGCGACATCAGCTGGAGATAACGACAAACACCGGTCAAG 263  
Qy 1007 ACTCCCGGACACCCAGGAGTGCCCTTAGAAAAAGCC-AAGCAAGTGTCTGAAATATTC 1065  
Db 262 ACTCCCGGACACCCAGGAGTGCCCTTAGAAAAAGCCAGGAGTGTCTGAAATATTC 203  
Qy 1066 AGTTCTTACAGCAGCAGACACCTCCATCTTCGACGACTTTGCTCTACGAGAGCGGCA- 1124  
Db 202 AGTTCTTACAGCAGCAGACACCTCCATCTTCGACGACTTTGCTCTACGAGAGCGGCA 143  
Qy 1125 GAGGAGGAGGAGTGTGGCGCAAGAACGGCAGAGTGGAAACAAATGAGGGCGAACC 1184  
Db 142 GAGGAGGAGGAGTGTGGCGCAAGAACGGCAGAGTGGAAACAAATGAGGGCGAACC 83  
Qy 1185 AGTTCTTACATGTTCTAAAGCTTTGACTTTTGAACACAGTTTAAACACAGTGTGCTTGGTC 1244  
Db 82 AGTTCTTACATGTTCTAAAGCTTTGACTTTTGAACACAGTTTAAACACAGTGTGCTTGGTC 23  
Qy 1245 AGTCCAGTGTGCTCGTCCCGTG 1266

Db 22 AGTCCAGTGTGCTCGTCTCGC 1

RESULT 38  
AA976117  
LOCUS

AA976117 460 bp mRNA linear EST 22-MAY-1998  
on33b10.s1 NCI\_CGAP\_Lu5 Homo sapiens cDNA clone IMAGE:1558459 3',  
mRNA sequence.

AA976117  
ACCESSION  
VERSION  
AA976117.1 GI:3151909  
KEYWORDS  
SOURCE  
EST.  
human.

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
1 (bases 1 to 460)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: rgap@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www.bio.lnlnl.gov/bbrp/image/image.html

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 439.

FEATURES

source

1..460  
/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="IMAGE:1558459"

/clone\_lib="NCI\_CGAP\_Lu5"

/tissue\_type="carcinoid"

/lab\_host="DH10B"

/notes="Organ: lung; Vector: p773D-Pac (Pharmacia) with a

modified polylinker; 1st strand cDNA was prepared from

neuroendocrine lung carcinoid, and was then primed with a

Not I - oligo(dT) primer. Double-stranded cDNA was ligated

to Eco RI adaptors (Pharmacia), digested with Not I and

cloned into the Not I and Eco RI sites of the modified

p7713 vector. Library is normalized. Library was

constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 123 a 78 c 79 g 180 t

ORIGIN

Query Match 22.5%; Score 456.8; DB 9; Length 460;

Best Local Similarity 99.8%; Pred. No. 1.4e-87;

Matches 459; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1402 TATCAATCAGATGATCTAATGTGAATGTAAGTATCTTAAAAACAAGCATCTATTTT 1461

Db 1 TATCAATCAGATGATCTAATGTGAATGTAAGTATCTTAAAAACAAGCATCTATTTT 60

Qy 1462 GGCAGAAATGTGTCTTAAATTCAGTCATTTGATATCTGTGAGACTTCATATTTCTCA 1521

Db 61 GGCAGAAATGTGTCTTAAATTCAGTCATTTGATATCTGTGAGACTTCATATTTCTCA 120

Qy 1522 TCCCTTTATTTGCTTTTTCAGCAACATAAGAACCATGAGTCATTTTTCATTAGATAT 1581

Db 121 TCCCTTTATTTGCTTTTTCAGCAACATAAGAACCATGAGTCATTTTTCATTAGATAT 180

Qy 1582 TCTGATAAAATCTCTTGAAAAATCTGAAATCAAAAGGTTAATGATTTTTTTTCTCATCTG 1641

Db 181 TCTGATAAAATCTCTTGAAAAATCTGAAATCAAAAGGTTAATGATTTTTTTTCTCATCTG 240

Qy 1642 ATTTGTCATTTTATATATCTGTTATTCGGTCTAAAGTGTAAATTTTACCATTGATTTTCT 1701



```
Db 241 ATTGTGCACTTTTATATCTGTTATCGGTCTAAAGTGTCTAATTTACCCATTGATTTTCT 300
QY 1702 GCTAGACAGATACTTTTAAATTTTTCAGATTTGGCAGACACTTTTCTTTTCTTTTGGAAA 1761
Db 301 GCTAGACAGATACTTTTAAATTTTTCAGATTTGGCAGACACTTTTCTTTTCTTTTGGAAA 360
QY 1762 ATCTTTCTTCCAGATCTGTGTGCGCACTGAACAGCACCCGTCCTCAGTCGTCTGGTGT 1821
Db 361 ATCTTTCTTCCAGATCTGTGTGCGCACTGAACAGCACCCGTCCTCAGTCGTCTGGTGT 420
QY 1822 CCGATTGGGCTGATGTTGTGGGGATGATGTGGAGG 1861
Db 421 CCGATTGGGCTGATGTTGTGGGGATGATGTGGAGG 460

RESULT 39
AL580786 778 bp mRNA linear EST 16-FEB-2001
LOCUS AL580786 LTI_NFL008_Tc2 Homo sapiens cDNA clone CS0DJ014YN09 5
DEFINITION prime, mRNA sequence.
ACCESSION AL580786
VERSION AL580786.1 GI:12947147
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 778)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1. .778
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DJ014YN09"
/clone_lib="LTI_NFL008_Tc2"
/sex="male"
/tissue_type="T cells from T cell leukemia"
/notes="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with NotI and
cloned into the NotI and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 187 a 102 c 246 g 187 t 56 others
ORIGIN
Query Match 22.2%; Score 450; DB 9; Length 778;
Best Local Similarity 93.0%; Pred. No. 3.7e-86;
Matches 452; Conservative 24; Mismatches 9; Indels 1; Gaps 1;

QY 1147 AGGAA CGCAGAGTGCAGAAACAATGAGCGGAGAACAGTCTTCTTACATGTTCTTAACGT 1206
Db 294 AGGAGCGGAGRTGGAAACAACAATGRCGGGGGRASSACTKCTTACATGKXSTAA CGK 353

QY 1207 TTGACTTTGAAAACAGTTTAAAACACGTGTGCTTGGTCAGCTCCAGTGTGTCGCCGTG 1266
Db 354 KTGRTSTTTGAAAACAGKTTAAAACACGKGGTGTGGKAGGTCCAGTGTGTCGCCGKG 413

QY 1267 CGGGGTTGAGTGTGATCTTTGCCCTTCTGTGCGTTGATTTTGCACAGATGATCTG 1326
Db 414 GGGGGTTGAGTGTGATCTTTGCCCTTCTGTGCGTTGATTTTGCACAGATGATCTG 473
```

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QY 1327 CATTATTTGTACTTTTCTATGTATTATAATCTGTAGAGTCACTAATAAGGAGTAT 1386
Db 474 CATTATTTGTACTTTTCTATGTATTATAATCTGTAGAGTCACTAATAAGGAGTAT 532
QY 1387 TTTTCTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAATGTAGTATCTTAAAAA 1446
Db 533 TTTTCTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAATGTAGTATCTTAAAAA 592
QY 1447 CAAAGCATCTATTTTGGCAGAAATGTGTCTTTAAATTCAGTCATTGTATTTCTGTAG 1506
Db 593 CAAAGCATCTATTTTGGCAGAAATGTGTCTTTAAATTCAGTCATTGTATTTCTGTAG 652
QY 1507 ACTTCATATTTCTATCCCTTTATTCCTTTTGTAGCAAAACATAGAACCATGAGTCATTT 1566
Db 653 ACTTCATATTTCTATCCCTTTATTCCTTTTGTAGCAAAACATAGAACCATGAGTCATTT 712
QY 1567 TGTCAATTTAGAGTATTTCTGATAAAATCTCTTGAATAATCTGAAATCAAAAGGTTAATGAT 1626
Db 713 TGTCAATTTAGAGTATTTCTGATAAAATCTCTTGAATAATCTGAAATCAAAAGGTTAATGAT 772
QY 1627 TTTTGTG 1632
Db 773 TTTTGTG 778

RESULT 40
AL524372 838 bp mRNA linear EST 13-FEB-2001
LOCUS AL524372 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC006YG03 3
DEFINITION prime, mRNA sequence.
ACCESSION AL524372
VERSION AL524372.1 GI:12787865
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 838)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1. .838
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC006YG03"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with NotI and
cloned into the NotI and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 248 a 164 c 131 g 207 t 28 others
ORIGIN
Query Match 22.0%; Score 445.2; DB 9; Length 838;
Best Local Similarity 92.4%; Pred. No. 3.9e-85;
Matches 453; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

QY 1539 AGCAACATAGAAACCATGAGTCATTTTGTCAATTAGAGTATCTTGATAAATCTCTTG 1598
```



Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
This read is a RESEQUENCE of a previously sequenced mouse clone  
This read has been verified (found to hit its original self in the  
correct orientation)

MG1:209275  
Seq primer: -40RP from Gibco  
High quality sequence stop: 463  
POLYA=No.

## FEATURES

Location/Qualifiers  
1..614  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:318659"  
/clone\_lib="Soares mouse p3NMF19.5"  
/dev\_stage="19.5 dpc total fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Vector: p773D (Pharmacia) with a modified  
polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGCGCGCATTTTCTTTTCTTTT 3']  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified p773 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M. Fatima Bonaldo. RNA was kindly provided by  
Dr. Minoru Ku (Wayne State University)."

BASE COUNT 169 a 136 c 163 g 144 t

## ORIGIN

Query Match 21.8%; Score 442.4; DB 9; Length 614;  
Best Local Similarity 86.3%; Pred. No. 1.6e-84;  
Matches 499; Conservative 0; Mismatches 78; Indels 1; Gaps 1;  
QY 667 GTGTTTCATCATCAAGAGCTACTGTAGGACGACATCCACCGCTCCATTAAGTACTCATC 726  
DB 2 GTGTTTCATCATCAAGAGCTATTCTGAGGACGACATCCACCGCTCCATCAAGTACTCATC 61  
QY 727 TGTGTAGCAGACGACGACACGCGCTGGACAGCGCTCCGCTCCATGACGACG 786  
DB 62 TGTGTAGTACTGAACACGCGCAACAGCGCTGGACGCGCTCCGCTCCATGACGACG 121  
QY 787 AAGGGGCGCTGTACCTGCTCTTCAAGGCTCAATGGGAGTGGGATTTTCTGGGGTGGCC 846  
DB 122 AAGGGGCTGTTTATCTCTCTTCAAGTGTCAATGGGAGTGGGATTTCTGTGGGGTGGCA 181  
QY 847 GAGATGAAGTCCCGGTGGACTACGGCACCAGTGC CGGGTCTGGTCTCAGGACAAAGTGG 906  
DB 182 GAGATGAAGTCCCGGTGGACTACGGCACCAGCGCTGGGCTGGTCTCAGGACAAAGTGG 241  
QY 907 AAGGGGAGTTTGTGTCAGTGGATTTTGTGAAGATGTACCAATACCAAGTCCGG 966  
DB 242 AAGGGAAAGTTTGTATGTGAAGTGGATTTTGTGAAGATGTGCCCCAACACCAAGTCCGG 301  
QY 967 CACATCAGGCTGGAGATTAACGACAAACCGGTACAAACTCCCGGGACACCCAGGAG 1026  
DB 302 CACATCAGATGGAGATTAACGACAAACCTGTGCAAACTCCCGTGTATACAGGAG 361  
QY 1027 GTGCCCTTAGAAAAGCAAGCAAGTGTCTGAAAATTTATCAGTTCTTCAAGCACACAAC 1086  
DB 362 GTGCCCTTAGAAAAGCAAAACAGTGTCTGAAGATTATCGCTTCTTATAAGCACACAAC 421  
QY 1087 TCCATCTTCAGCAGCTTTGCTCTACTACGAGAGCGCA -GAGGAGGAGGAGGTGGTCCG 1145  
DB 422 TCTATCTTTCAGCAGCTTTTCTCTATTATGAGAGCGCCAGGAGGAGGAGGTGGTCCGT 481  
QY 1146 AAGGAACGCGAGTCCGAAACAAACATAGGGCGAACCAAGTCTTCTTACATGTTCTAACG 1205  
DB 482 AAGGAAGACAGAAATCGAAACAAACAAATAGAAACAAGCCAGTTTGTGTTTAAATGGT 541  
QY 1206 TTTGACTTTGAAAACAGTTTAAAAACAGGTGTGCTTGGT 1243

DB 542 TGACNTGAAAACAGAGTTNTAAAGCTGTATGCTTGGT 579  
RESULT 43  
BO421488 902 bp mRNA linear EST 23-MAY-2002  
LOCUS AGENCOURT 7771914 NIH\_MGC\_92 Homo sapiens cDNA clone IMAGE:6014712  
DEFINITION 5', mRNA sequence.  
ACCESSION BO421488  
VERSION BO421488.1 GI:21116803  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 902)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL3209 row: k column: 01  
High quality sequence stop: 444.  
Location/Qualifiers  
1..902  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6014712"  
/clone\_lib="NIH\_MGC\_92"  
/tissue\_type="embryonal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: Not 1;  
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 2.5 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

BASE COUNT 242 a 219 c 288 g 132 t

## ORIGIN

Query Match 21.7%; Score 439.4; DB 14; Length 902;  
Best Local Similarity 99.8%; Pred. No. 6.8e-84;  
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 651 TCTGAAAAGCGGCGTGTTCATCATCAAGAGCTACTCTGAGGACGACATCCACCGCTC 710  
DB 1 TCTGAAAAGCGGCGTGTTCATCATCAAGAGCTACTCTGAGGACGACATCCACCGCTC 60  
QY 711 CATTAAGTACTCCATCTGCTGTAGCAGAGCAGCGCAACAGCGCTGGACAGCGCTT 770  
DB 61 CATTAAGTACTCCATCTGCTGTAGCAGAGCAGCGCAACAGCGCTGGACAGCGCTT 120  
QY 771 CCGCTGCATGAGCAGCAAGGGCGCGTCTACCTGCTCTTCAGGCTCAATGGGAGTGGCA 830  
DB 121 CCGCTGCATGAGCAGCAAGGGCGCGTCTACCTGCTCTTCAGGCTCAATGGGAGTGGCA 180  
QY 831 TTTTTCGTGGGGTGGCGAGATGAAGTCCCGGTGGACTACGGCACCAGTCCCGGGGTCTG 890  
DB 181 TTTTTCGTGGGGTGGCGAGATGAAGTCCCGGTGGACTACGGCACCAGTCCCGGGGTCTG 240  
QY 891 GTCTCAGGACAAAGTGAAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGATGTACC 950  
DB 241 GTCTCAGGACAAAGTGAAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGATGTACC 300  
QY 951 CAATAACCAAGTCCCGCAGATCAAGGCTGGAGATATACGACAAACCAACCGGTCAAACTC 1010

```

Db 301 CAATAACGAGCTCCGGACATCAGGCTGGAGAAATACAGACAAACCCGGTCACAAATC 360
Qy 1011 CCGGACACCCAGGAGTGCCTTTAGAAAAAGCCAAAGCAAGTGTGCTGAAATATCAGTTC 1070
Db 361 CCGGACACCCAGGAGTGCCTTTAGAAAAAGCCAAAGCAAGTGTGCTGAAATATCAGTTC 420
Qy 1071 CTACAAGCACACCTCCAT 1091
Db 421 CTACAAGCACACCTCCAT 441

RESULT 44
BM556661
LOCUS BM556661 977 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT 6540480 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737877
5', mRNA sequence.
ACCESSION BM556661
VERSION BM556661.1 GI:18798067
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 977)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.lnl.gov
Plate: LMNL2748 row: 1 column: 06
High quality sequence stop: 715.
FEATURES
source
1..977
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5737877"
/clone_lib="NIH_MGC_88"
/tissue_types="duodenal adenocarcinoma, cell line"
/lab_hosts="DH10B (phage-resistant)"
/notes="Organ: small intestine; Vector: pCMV-SPORT6;
Site:1: NotI; Site:2: SalI; Cloned unidirectionally;
oligo-dr primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH MGC library."
BASE COUNT 255 a 182 c 203 g 335 t
ORIGIN
Query Match 21.4%; Score 434.4; DB 13; Length 977;
Best Local Similarity 99.6%; Pred. No. 8e-83;
Matches 446; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1581 TTCTGATAAATCTCTGAAATCTGAATCAAAAGGTTAATGATTTTTTTGTCATCT 1640
Db 49 TTCTGATAAATCTCTGAAATCTGAATCAAAAGGTTAATGATTTTTTTGTCATCT 108
Qy 1641 GATTGTGCAATTTATATCTGTTATCGGTCTAAAGTGTCTAATTTACCCATTTGATTTTC 1700
Db 109 GATTGTGCAATTTATATCTGTTATCGGTCTAAGTGTCTAATTTACCCATTTGATTTTC 168
Qy 1701 TGCTAGACAGATACTTTTAATTTTCAAAATTTGGCAGACACTTTTTTTTTTTTGA 1760
Db 169 TGCTAGACAGATACTTTTAATTTTCAAAATTTGGCAGACAC-TTTTTTTTTTTTGA 227
Qy 1761 AATCTTTCTCCAGATCTGTTGCCACTGAACGCCACCGCTCCCTCACTGCTCGTG 1820
Db 228 AATCTTTCTCCAGATCTGTTGCCACTGAACGCCACCGCTCCCTCACTGCTCGTG 287

```

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Qy 1821 TCCGATTGGGCTGGATGGTGTGGGGCATGATGTGTGAGGAACTGGAAAGTGTCTTTAGG 1880
Db 288 TCCGATTGGGCTGGATGGTGTGGGGCATGATGTGTGAGGAACTGGAAAGTGTCTTTAGG 347
Qy 1881 TCTGGTTCCAGGTCGGGCATCTTTGTTGTTTGCACATCTTTTAAATTTTACACCTTTT 1940
Db 348 TCTGGTTCCAGGTCGGGCATCTTTGTTGTTTGCACATCTTTTAAATTTTACACCTTTT 407
Qy 1941 CTTAAGAATTTCTAATGCGCTTAAAGTTTTTATACCAATTAATGCTGAGCTTTAAGTGTAG 2000
Db 408 CTTAAGAATTTCTAATGCGCTTAAAGTTTTTATACCAATTAATGCTGAGCTTTAAGTGTAG 467
Qy 2001 GATCTGCTAGTACAGACAGTGTGATGGA 2028
Db 468 GATCTGCTAGTACAGACAGTGTGATGGA 495

RESULT 45
BM745209
LOCUS BM745209 435 bp mRNA linear EST 01-MAR-2002
DEFINITION K-EST0019027 S5SNU484 Homo sapiens cDNA clone S5SNU484-16-B11 5',
mRNA sequence.
ACCESSION BM745209
VERSION BM745209.1 GI:19066538
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 435)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 16 row: B column: 11
High quality sequence stop: 435.
FEATURES
source
1..435
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S5SNU484-16-B11"
/clone_lib="S5SNU484"
/sex="M"
/tissue_type="Stomach"
/cell_type="Epithelial"
/lab_hosts="Top10f"
/notes="Organ: Stomach; Vector: pTZ18Rpl; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was decapped with tabacco
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
including EcoRI site by treatment of 14 RNA ligase. The
first strand cDNA was synthesized from oligo dt-selected
mRNA by priming with dt-tailed vector. The dt-tailed
vector was adjusted to have about 60nt. The cDNA vector
was circularized with E. coli DNA ligase after digestion
of EcoRI which site is also included in vector. An RNA
strand converted to a DNA strand by Okayama-Berg method.
The obtained cDNA vectors were used for transformation of
competent cells E. coli Top10f, by electroporation
method."
BASE COUNT 102 a 142 c 116 g 75 t
ORIGIN
Query Match 21.3%; Score 431; DB 14; Length 435;

```

Best Local Similarity 100.0%; Pred. No. 4.6e-82; Mismatches 0; Indels 0; Gaps 0; Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 400 GCTCAGGCTCTCCAGCAGACGCCCGCTTGGCTCAACCGCAGTATCAGAGCCCTCAG 459
Db 5 GCTCAGGCTCTCCAGCAGACGCCCGCTTGGCTCAACCGCAGTATCAGAGCCCTCAG 64
QY 460 CAGCCACCCAGACCCGCTGGGTTGGCCCAAGCAACAAAGAAACCGCGGTTGGGCGAGC 519
Db 65 CAGCCACCCAGACCCGCTGGGTTGGCCCAAGCAACAAAGAAACCGCGGTTGGGCGAGC 124
QY 520 GAGGGGCTGGCAGCGATAGCACTCTCCGGAACGCTCAGGCTAATCTTGCCCGCAGC 579
Db 125 GAGGGGCTGGCAGCGATAGCACTCTCCGGAACGCTCAGGCTAATCTTGCCCGCAGC 184
QY 580 GTCGAATCCCAACCCCGCTTGAAGAACTGAAGGCTCTCAGCAGCTACAAACCCGAAAGAG 639
Db 185 GTCGAATCCCAACCCCGCTTGAAGAACTGAAGGCTCTCAGCAGCTACAAACCCGAAAGAG 244
QY 640 TTTGAGTGGAACTGAAAGCGGGCGTGTTCATCATCAAGAGCTACTCTGAGGAGCAGC 699
Db 245 TTTGAGTGGAACTGAAAGCGGGCGTGTTCATCATCAAGAGCTACTCTGAGGAGCAGC 304
QY 700 ATCAGCGCTCCATTAAGTACTCTGAGCAGCAAGCGGCGTGTTCATCATCAAGAGCTACTCTGAGGAGCAGC 759
Db 305 ATCAGCGCTCCATTAAGTACTCTGAGCAGCAAGCGGCGTGTTCATCATCAAGAGCTACTCTGAGGAGCAGC 364
QY 760 GACAGCGCTTCGCTGATGAGCAGCAAGCGGCGTGTTCATCATCAAGAGCTACTCTGAGGAGCAGC 819
Db 365 GACAGCGCTTCGCTGATGAGCAGCAAGCGGCGTGTTCATCATCAAGAGCTACTCTGAGGAGCAGC 424
QY 820 GGGAGTGGGCA 830
Db 425 GGGAGTGGGCA 435
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## RESULT 46

BI224711  
LOCUS 602949342F1 NIH\_MGC\_8 Homo sapiens cDNA clone IMAGE:5093698 5',  
DEFINITION mRNA sequence.

ACCESSION BI224711

VERSION BI224711.1 GI:14678155

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 623)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: L1CM1861 row: c column: 11

High quality sequence stop: 584.

## FEATURES

source

1. .623

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5093698"

/clone\_lib="NIH MGC 8"

/tissue\_type="Burkitt lymphoma"

/lab\_host="DHI08 (phage-resistant)"

/note="Organ: lymph; Vector: pOT7; Site:1: XhoI; Site\_2:

ECORI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 179 a 141 c 155 g 148 t

## ORIGIN

Query Match 21.2%; Score 430.8; DB 13; Length 623;

Best Local Similarity 89.5%; Pred. No. 4.9e-82;

Matches 544; Conservative 0; Mismatches 52; Indels 12; Gaps 7;

QY 857 CCCCCTGAGTACGGCACAGTCCGGGCTCTGCTCAGGACAAAGTGAAGGGGAAGT 916

Db 2 CCCCCTGAGTACGGCACAGTCCGGGCTCTGCTCAGGACAAAGTGAAGGGGAAGT 61

QY 917 TTGATCTCCAGTGGATTTTGTAAAGGATGACCCCAATACCCAGCTCCGCACATCAGGC 976

Db 62 TTGATCTCCAGTGGATTTTGTAAAGGATGACCCCAATACCCAGCTCCGCACATCAGGC 121

QY 977 TGGAGAAATAACGACAAACACCGGTCAAACTCCCGGACACCCAGAGGTCCTCTTAG 1036

Db 122 TGGAGAAATAACGACAAACACCGGTCAAACTCCCGGACACCCAGAGGTCCTCTTAG 181

QY 1037 AAAAGCCAAAGCAAGTGTGAAAATTTATCAGTTCCTCAAGCACACAACCTCCATCTTCG 1096

Db 182 AAAAGCCAAAGCAAGTGTGAAAATTTATCAGTTCCTCAAGCACACAACCTCCATCTTCG 241

QY 1097 ACAGCTTGTCTACTACGAGAACCGCA-GAGGAGGAGGAGTGGTCCGACAGGAAGGC 1155

Db 242 ACAGCTTGTCTACTACGAGAACCGCA-GAGGAGGAGGAGTGGTCCGACAGGAAGGC 301

QY 1156 AGAGTCGAAACAAACCAATGAGGCGAAACAGTTCTTACA---TGTTCTAACTTTGACT 1212

Db 302 AGAGTCGAAACAAACCAATGAGGCGAAACAGTTCTTACA---TGTTCTAACTTTGACT 361

QY 1213 TTGAAACACAG---TTTAAACACAGTGTGTCTGCTCAGCTCCAG-TGTGTCTCCCGTGG 1268

Db 362 TTGAAACACAGTTTAAACACAGTGTGTCTGCTCAGCTCCAGATGTGTCTCCCGTGG 421

QY 1269 GGGGTTGA-GGTGTGATCTTTGCCCTT-TCCTGTCTGTGAT-TTTTCCCGACATGATC 1324

Db 422 GGGGTTGACGTGTAGCATCTTTGCCCTTATCTTGTCTGTATATATATGTCAGATGATC 481

QY 1325 TGCAATTTATTTGACTTTTCTATGATTAATACTCTGTAGAGTCACTAATAAGAGGT 1384

Db 482 TGCAATTTATTTGACTTTTCTATGATTAATACTCTGTAGAGTCACTAATAAGAGGT 541

QY 1385 ATTTTGTGTGAGCTTATCAATCAGACTGATCTAATGTGAAATGTAGTATCCTTTAA 1444

Db 542 CATACCACCGTCCAGCTTATCAATCAGACTGATCTAATGTGAAATGTAGTATCCTTTAA 601

QY 1445 ACAAAGC 1452

Db 602 CACACAC 609

RESULT 47

R69898

LOCUS y147a01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone

DEFINITION IMAGE:142344 5', mRNA sequence.

ACCESSION R69898

VERSION R69898.1 GI:843415

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 629)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: L1CM1861 row: c column: 11

High quality sequence stop: 584.

FEATURES

source

1. .623

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5093698"

/clone\_lib="NIH MGC 8"

/tissue\_type="Burkitt lymphoma"

/lab\_host="DHI08 (phage-resistant)"

/note="Organ: lymph; Vector: pOT7; Site:1: XhoI; Site\_2:

ECORI; cDNA made by oligo-dT priming. Directionally

Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.

TITLE  
JOURNAL  
COMMENT

Unpublished (1995)  
Contact: Wilton RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

Insert Size: 957  
High quality sequence stops: 381  
Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 957 Std Error: 0.00  
Seq primer: M13p1  
High quality sequence stop: 381.

Location/Qualifiers  
1. 629

FEATURES  
source

/organism="Homo sapiens"  
/db\_xref="GDB:551383"  
/db\_xref="taxon:9606"  
/clone="IMAGE:142344"  
/clone\_lib="Soares placenta Nb2HP"  
/sex="Female"  
/dev\_stage="placenta obtained at birth (full term)"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: placenta; Vector: p7T3D (Pharmacia) with a  
modified polylinker; Site: 1; Not 1; Site 2: Eco RI; 1st [5'  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
AATCGAAGATTCGGCCGCGCAGGAATTTTTTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p7T3 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 144 a 101 c 139 g 238 t 7 others  
ORIGIN

Query Match 21.0%; Score 426; DB 14; Length 629;

Best Local Similarity 97.8%; Pred. No. 5.3e-81; Length 629;  
Matches 452; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

Qy 1568 GTCATTAGAGTATCTGATAAAATCTCTTGAATACTGAAATCAAAGGTTAATGATT 1627

Db 11 GGCATTAGAGTATCTGATAAAATCTCTTGAATACTGAAATCAAAGGTTAATGATT 70

Qy 1628 TTTGTTCAATCTGATTTGTCATTTATATCTGTTATCTGTTGCTTAAAGTCTAATTTACC 1687

Db 71 TTTTGTTCATTTCTGATTTGTCATTTTATATCTGTTATCTGTTGCTTAAAGTCTAATTTACC 130

Qy 1688 CATTTGATTTTCTCTAGACAGATAACTTTTAAATTTTCAAATTTTGGCAGACACTTTT 1747

Db 131 CATTTGATTTTCTCTAGACAGATAACTTTTAAATTTTCAAATTTTGGCAGACACTTTT 190

Qy 1748 TTTTTTTTGGAAATCTTTCTCCAGATCTGTTGCCACTGAAACAGCCACCCCTCCCT 1807

Db 191 TTTTTTTTGGAAATCTTTCTCCAGATCTGTTGCCACTGAAACAGCCACCCCTCCCT 250

Qy 1808 CACTGCTCTGTTGCCGATTTGGGCTGGATGTTGTTGGGGCATGATGTTGGAGGAACCTGG 1867

Db 251 CACTGCTCTGTTGCCGATTTGGGCTGGATGTTGTTGGGGCATGATGTTGGAGGAACCTGG 310

Qy 1868 AAGTGCTTTAGGCTGCTGCTGAGGCTGGGCAATCTTTGTTGTTGGCATCTTTTAAA 1927

Db 311 AAGTGCTTTAGGCTGCTGCTGAGGCTGGGCAATCTTTGTTGTTGGCATCTTTTAAA 370

Qy 1928 TTTTACACCTTTTCTTAAGAATT--CTAATGCCGCTCTTAAGTTTATATCAATTAATGCT 1985

Db 371 TTTTACACCTTTTCTTAAGAATTTCTAATGCCGCTCTTAAGTTTATATCAATTAATGCT 429

Qy 1986 GAGCTTTAAGTGTAGGATCTGTGTATACAGACAGTGTGATGG 2027

Db 430 GAGCTTTAAGTGTAGGATCTGTGTATACAGACAGTGTGATGG 471

RESULT 48

BJ044639/c

LOCUS

DEFINITION

laevis cDNA clone XL013p15 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Xenopus laevis

African clawed frog.

Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 687)

REFERENCE

AUTHORS

Kitayama, A., Terakawa, C., Mochii, M., Ueno, N., Shin-1, T. and Kohara

Y.

Expressed genes in X. laevis embryo

Unpublished (2001)

Contact: Tadasu Shin-1

Contact For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tehini@genes.nig.ac.jp.

Location/Qualifiers

1. 687

/organism="Xenopus laevis"

/db\_xref="taxon:8385"

/clone="XL013p15"

/clone\_lib="NIBB Mochii normalized Xenopus neurula

library"

/tissue\_type="whole embryo"

/dev\_stage="stage 15"

/note="Vector: pBSRN3; Site: 1; Not1; Site: 2: EcoRI; cDNAs

were oligo-dT primed and directionally cloned. Staging

according to Newkooop and Faber. Library is substracted

and was constructed by N. Garrett and A.M. Zorn,

(Wellcome/CRC Institute). "

BASE COUNT 142 a 170 c 182 g 193 t

ORIGIN

Query Match 20.9%; Score 424.4; DB 13; Length 687;

Best Local Similarity 82.9%; Pred. No. 1.2e-80;

Matches 496; Conservative 0; Mismatches 101; Indels 1; Gaps 1;

Qy 559 CAGCCTAATTCGCCCCCGCGTCGAATCCACCCCGTCCTTGAAACACTGAAGGCTGCT 618

Db 687 CAGTCTCAGCGTCGCCCGGAAATGAGTCTCACCTCTGCTAGAGAACTGAAGGCCGCC 628

Qy 619 CACAGCTACAAACCCGAAAGAGTTTGAAGTGAATCTGAAAACGGCGGCTGTTTATCATC 678

Db 627 CACAGCTACAAACCCGAAAGAGTTTGAAGTGAATCTGAAAACGGCGGCTGTTTATCATC 568

Qy 679 AAGAGCTACTCTGAGGAGGACATCCAGCGCTCCATTAAGTACTCCATCTGCTGTAGCACA 738

Db 567 AAGAGCTACTCTGAGGAGGATATCCACGTTCCATTAAGTACTCCATCTGCTGTAGCACA 508

Qy 739 GAGCACGGCAACAAAGCGCCTGGACAGCGCCCTTCGCTGCATGAGCAGCAAGGGGCCCTC 798

Db 507 GAGCATGGGAATAACGCTTGATAACGCTTTCGCTCCATGAATGGCAAGGCCCTC 448

Qy 799 TACCTGCTCTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCCGAGATGAAGTCC 858

Db 447 TACCTGCTCTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCCGAGATGAAGTCC 388

Qy 859 CCCGTGGACTACGCCACCGAGTCCGGGCTGTGCTCTCAGGACAAGTGAAGGGAAGTTT 918

Db 387 CCCGTGGATTATGGCACCCAGTCCGGGCTGTGCTCTCAGGACAAGTGAAGGGAAGTTT 328

```
QY 919 GATGTCAGTGGATTTTGTAAAGGATGACCAATAACCAAGCTCCGGCACATCAGGCTG 978
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 327 GAGTCAAGTGGCTCTTTGTCAAGGAGCTTCCCAACAACCAAGCTGAGGCACATCCGCTG 268
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 979 GAGAATAACGACAACAACCGGTACAAATCCCGGGACACCCAGGAGGTGCCCTTAGAA 1038
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 GAGAATAACGACAACAACCGGTACAAATCCCGGGACACCCAGGAGGTGCCCTTAGAA 208
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1039 AAGCCCAAGCAAGTGTGAAATATACAGTTCTCAAGCACACAACCTCCATCTTCGAC 1098
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 207 AAGCAAAACGTGTGCTTAAATATCATTTGCCACTTTCAAGCACACAGCCTCCATCTTTGAT 148
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1099 GACTTTGCTCACTACGAGAGCGCCA-GAGGAGGAGGAGGTGTGGCGAAGGAACCGC 1155
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 147 GACTTTTCTCATACGAGAGCGCGAGGAGGAGGAGGTGTGGCGAAGGTAACGC 90
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 49
AI083909/c 449 bp mRNA linear EST 10-NOV-1998
LOCUS qf26b05.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:1751121 3'
DEFINITION similar to TR:004503 004503 SEQUENCE OF BAC F21M12 FROM ARABIDOPSIS
THALIANA CHROMOSOME 1, COMPLETE SEQUENCE. ;, mRNA sequence.
ACCESSION AI083909
VERSION AI083909.1 GI:3422332
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 449)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGA), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1946 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 418.
FEATURES
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1751121"
/clone_lib="NCI CGAP Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_hosts="Dh10B"
/notes="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAGTGGGAGCGCGCATAGTATTTTATTTTATTTTATTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 120 a 106 c 100 g 123 t
ORIGIN

QY 960 GCTCCGGCACATCAGGCTGGAGATAACGACAACAACCGGTACAAACTCCCGGACAC 1019
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 449 GCTCCGGCACATCAGGCTGGAGATAACGACAACAACCGGTACAAACTCCCGGACAC 390
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1020 CCAGAGGTGCCCTTAGAAAAAGCCAAAGCAAGTGTCTGAAAAATTATCAGTTCTTACAAGCA 1079
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 389 CCAGAGGTGCCCTTAGAAAAAGCCAAAGCAAGTGTCTGAAAAATTATCAGTTCTTACAAGCA 330
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1080 CACAACCTCCATCTTCGACGACTTTGCTCACTACGAGAAAGCGCCA-GAGGAGGAGGAGGT 1138
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 329 CACAACCTCCATCTTCGACGACTTTGCTCACTACGAGAAAGCGCCAAGGAGGAGGT 270
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1139 GTGGCGCAAGGAACGGCAGAGTCGAAACAACAATGAGGGCGAAACAGTTTCTTACATGT 1198
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 269 GTGGCGCAAGGAACGGCAGAGTCGAAACAACAATGAGGGCGAAACAGTTTCTTACATGT 210
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1199 TCTAACCTTTGACTTTGAAAAACAGTTTAAAAACAGTGTGCTTGGTCAGCTCCAGTGTGC 1258
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 209 TCTAACCTTTGACTTTGAAAAACAGTTTAAAAACAGTGTGCTTGGTCAGCTCCAGTGTGC 150
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1259 GTCCCGTGGCGGGGTGAGTGTTCATCTTTGCTTCTTCTGTTGATTTTGGCCACA 1318
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 149 GTCCCGTGGCGGGGTGAGTGTTCATCTTTGCTTCTTCTGTTGATTTTGGCCACA 90
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1319 TGGATCTGCATTTATTTGACTTTTCTTATGTATTATATCTCTAGAAAGTCACTAATAA 1378
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89 TGGATCTGCATTTATTTGACTTTTCTTATGTATTATATCTCTAGAAAGTCACTAATAA 30
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1379 AGAGATATTTTGTTCAGCTTATCAA 1407
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 29 AGAGATATTTGTTCAGCTTATCAA 2
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 50
AW387755/c 435 bp mRNA linear EST 04-FEB-2000
LOCUS MR4-ST0118-041099-010-A06 ST0118 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW387755
ACCESSION AW387755
VERSION AW387755.1 GI:6892414
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 435)
HGCP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC0&t2=MR4-ST0118-
041099-010-A06&t3=1999-10-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 434.
FEATURES
source
1. .435
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0118"
/dev_stage="Adult"
/notes="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
```

```
Matches 446; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY 960 GCTCCGGCACATCAGGCTGGAGATAACGACAACAACCGGTACAAACTCCCGGACAC 1019
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 449 GCTCCGGCACATCAGGCTGGAGATAACGACAACAACCGGTACAAACTCCCGGACAC 390
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1020 CCAGAGGTGCCCTTAGAAAAAGCCAAAGCAAGTGTCTGAAAAATTATCAGTTCTTACAAGCA 1079
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 389 CCAGAGGTGCCCTTAGAAAAAGCCAAAGCAAGTGTCTGAAAAATTATCAGTTCTTACAAGCA 330
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1080 CACAACCTCCATCTTCGACGACTTTGCTCACTACGAGAAAGCGCCA-GAGGAGGAGGAGGT 1138
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 329 CACAACCTCCATCTTCGACGACTTTGCTCACTACGAGAAAGCGCCAAGGAGGAGGT 270
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1139 GTGGCGCAAGGAACGGCAGAGTCGAAACAACAATGAGGGCGAAACAGTTTCTTACATGT 1198
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 269 GTGGCGCAAGGAACGGCAGAGTCGAAACAACAATGAGGGCGAAACAGTTTCTTACATGT 210
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1199 TCTAACCTTTGACTTTGAAAAACAGTTTAAAAACAGTGTGCTTGGTCAGCTCCAGTGTGC 1258
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 209 TCTAACCTTTGACTTTGAAAAACAGTTTAAAAACAGTGTGCTTGGTCAGCTCCAGTGTGC 150
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1259 GTCCCGTGGCGGGGTGAGTGTTCATCTTTGCTTCTTCTGTTGATTTTGGCCACA 1318
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 149 GTCCCGTGGCGGGGTGAGTGTTCATCTTTGCTTCTTCTGTTGATTTTGGCCACA 90
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1319 TGGATCTGCATTTATTTGACTTTTCTTATGTATTATATCTCTAGAAAGTCACTAATAA 1378
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89 TGGATCTGCATTTATTTGACTTTTCTTATGTATTATATCTCTAGAAAGTCACTAATAA 30
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1379 AGAGATATTTTGTTCAGCTTATCAA 1407
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 29 AGAGATATTTGTTCAGCTTATCAA 2
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 50
AW387755/c 435 bp mRNA linear EST 04-FEB-2000
LOCUS MR4-ST0118-041099-010-A06 ST0118 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW387755
ACCESSION AW387755
VERSION AW387755.1 GI:6892414
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 435)
HGCP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=RC0&t2=MR4-ST0118-
041099-010-A06&t3=1999-10-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 434.
FEATURES
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1. .435
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0118"
/dev_stage="Adult"
/notes="Organ: stomach; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
```



No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 19 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions "

```
BASE COUNT      90 a   121 c   104 g   120 t
ORIGIN

Query Match      20.6%; Score 418.2; DB 10; Length 435;
Best Local Similarity 99.1%; Pred. No. 2.6e-79;
Matches 431; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 841 GTGCCGAGATGAATGCCCGTGGAGCTACGGACACAGTGGCGGGGTCTGTCTCAGGAC 900
Db 435 GTGCCGAGATGAATGCCCGTGGAGCTACGGACACAGTGGCGGGGTCTGTCTCAGGAC 376

Qy 901 AAGTGGAGGGGAAGTTTGATGCTCAGTGGATTTTGTGTTAAGGATGTACCCCAATACCG 960
Db 375 AAGTGGAGGGGAAGTTTGATGCTCAGTGGATTTTGTGTTAAGGATGTACCCCTATACCG 316

Qy 961 CTCGGCACATCAGGCTGGAGATAACGACAAACACCGGTCACAAACTCCCGGGACACC 1020
Db 315 CTCGACACATCAGGCTGGAGATAACGACAAACACCGGTCACAAACTCCCGGGACACC 256

Qy 1021 CAGAGGTGCCCTTAGAAAAAGCAAGCAAGTGTGTAATAATTCAGTTCTCTACAGGAC 1080
Db 255 CAGAGGTGCCCTTAGAAAAAGCCTAGCAAGTGTGTAATAATTCAGTTCTCTACAGGAC 196

Qy 1081 ACAACCTCCATCTTCGAGCACTTTCCTACACGAGAGAGAGAGAGAGAGAGAGAGAG 1139
Db 195 ACAACCTCCATCTTCGAGCACTTTCCTACACGAGAGAGAGAGAGAGAGAGAGAGAG 136

Qy 1140 GTGCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1199
Db 135 GTGCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 76

Qy 1200 CTAACGTTTGACTTTGAAAAAGAGTTTAAACACAGTGTGCTTGGTCAGCTCCAGTGTGCG 1259
Db 75 CTAACGTTTGACTTTGAAAAAGAGTTTAAACACAGTGTGCTTGGTCAGCTCCAGTGTGCG 16

Qy 1260 TCCCGTGGGGGGTT 1274
Db 15 TCCCGTGGGGGGTT 1

RESULT 51
AV725141
LOCUS      AV725141      429 bp      mRNA      linear      EST 16-OCT-2000
DEFINITION      AV725141      HTC Homo sapiens cDNA clone HTCAMH07 5', mRNA sequence.
ACCESSION      AV725141
VERSION      AV725141.1      GI:10830231
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu
S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA HTC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1. .429
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="HTCAMH07"
/clone_lib="HTC"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT      125 a   59 c   57 g   188 t
ORIGIN

Query Match      20.6%; Score 418; DB 10; Length 429;
Best Local Similarity 99.8%; Pred. No. 2.8e-79;
Matches 429; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1329 TTTTATTTGTAATTTTCTATGATTAATAAATCCCTGCTAGAGTCACATAAAGGAGTATTT 1308
Db 1 TTTTATTTGTAATTTTCTATGATTAATAAATCCCTGCTAGAGTCACATAAAGGAGTATTT 59

Qy 1389 TTTTATTTGTAATTTTCTATGATTAATAAATCCCTGCTAGAGTCACATAAAGGAGTATTT 1448
Db 60 TTTTATTTGTAATTTTCTATGATTAATAAATCCCTGCTAGAGTCACATAAAGGAGTATTT 119

Qy 1449 AAGCATCTATTTTGGCAGAAATTTGTGTTCTTAAATTCAGTCATTTTGATATCTGTGAGAC 1508
Db 120 AAGCATCTATTTTGGCAGAAATTTGTGTTCTTAAATTCAGTCATTTTGATATCTGTGAGAC 179

Qy 1509 TTTATATTTCTCATCCCTTTTATGCTTTTGTAGCAACATAGAAACCATCAGTCATTTTG 1568
Db 180 TTTATATTTCTCATCCCTTTTATGCTTTTGTAGCAACATAGAAACCATCAGTCATTTTG 239

Qy 1569 TCATTTAGAGTATTTCTGATAAAATCTCTGAAATCTGAAATCAAAAGGTTAATGATTT 1628
Db 240 TCATTTAGAGTATTTCTGATAAAATCTCTGAAATCTGAAATCAAAAGGTTAATGATTT 299

Qy 1629 TTTGTTCAATTTGATTTGTGATTTATATCTGTTATCGGTCTAAAGTGCTAATTTTACCC 1688
Db 300 TTTGTTCAATTTGATTTGTGATTTATATCTGTTATCGGTCTAAAGTGCTAATTTTACCC 359

Qy 1689 ATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTTT 1748
Db 360 ATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTTT 419

Qy 1749 TTTTATTTTGG 1758
Db 420 TTTTATTTTGG 429

RESULT 52
AV729447
LOCUS      AV729447      429 bp      mRNA      linear      EST 17-OCT-2000
DEFINITION      AV729447      HTC Homo sapiens cDNA clone HTCAMF05 5', mRNA sequence.
ACCESSION      AV729447
VERSION      AV729447.1      GI:10838868
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu
S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA HTC clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
```



This clone is available at CHGC in Shanghai.

# FEATURES

source  
1..429  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="HTCAMP05"  
/clone\_lib="HTC"  
/tissue\_type="Hypothalamus"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 125 a 59 c 57 g 188 t  
ORIGIN  
Query Match 20.6%; Score 418; DB 10; Length 429;  
Best Local Similarity 99.8%; Pred. No. 2.8e-79;  
Matches 429; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1329 TTTATTGTACCTTTTCTATGATTAATAATCCCTGTAGAAGTCATAATAAAGAGTATTT 1388  
DB 1 TTTATTGTACCTTTTCTATGATTAATAATCCCTGTAGAAGTCATAATAAAGAGTATTT 59  
QY 1389 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 1448  
DB 60 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 119  
QY 1449 AAGCATCTATTTGGCAGAAATGTCTTCTTAATTCAGTCATTTGATATTCGTGAGAC 1508  
DB 120 AAGCATCTATTTGGCAGAAATGTCTTCTTAATTCAGTCATTTGATATTCGTGAGAC 179  
QY 1509 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 1628  
DB 240 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 259  
QY 1629 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 1688  
DB 300 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 359  
QY 1689 ATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTTT 1748  
DB 360 ATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTTT 419  
QY 1749 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 1758  
DB 420 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 429

RESULT 53  
AV729585  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AV729585 HTC Homo sapiens cdna clone HTCANC06 5', mRNA linear EST 17-OCT-2000  
AV729585  
AV729585.1 GI:10839006  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
CONTACT  
JOURNAL  
COMMENT

1 (bases 1 to 429)  
Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,  
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu,  
S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,  
Chen, J., Chen, Z., and Han, Z.  
Homo sapiens cdna HTC clones  
Unpublished (2000)  
Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.

# FEATURES

source  
1..429  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="HTCANC06"  
/clone\_lib="HTC"  
/tissue\_type="Hypothalamus"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 125 a 59 c 57 g 188 t  
ORIGIN  
Query Match 20.6%; Score 418; DB 10; Length 429;  
Best Local Similarity 99.8%; Pred. No. 2.8e-79;  
Matches 429; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1329 TTTATTGTACCTTTTCTATGATTAATAATCCCTGTAGAAGTCATAATAAAGAGTATTT 1388  
DB 1 TTTATTGTACCTTTTCTATGATTAATAATCCCTGTAGAAGTCATAATAAAGAGTATTT 59  
QY 1389 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 1448  
DB 60 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 119  
QY 1449 AAGCATCTATTTGGCAGAAATGTCTTCTTAATTCAGTCATTTGATATTCGTGAGAC 1508  
DB 120 AAGCATCTATTTGGCAGAAATGTCTTCTTAATTCAGTCATTTGATATTCGTGAGAC 179  
QY 1509 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 1628  
DB 240 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 259  
QY 1629 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 1688  
DB 300 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 359  
QY 1689 ATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTTT 1748  
DB 360 ATTTGATTTTCTGCTAGACAGATACTTTTAAATTTTCAAAATTTGGCAGACACTTTTTT 419  
QY 1749 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 1758  
DB 420 TTTTGTGAGCTTATCAATCAGACTGATCTAATGTGAAGTGAAGTATCCTTTAAAAACA 429

# RESULT 54

AV729585  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AV729585 NIBB Mochii normalized Xenopus neurula library Xenopus laevis cdna clone XLO13e02 3', mRNA sequence.  
AV729585  
AV729585.1 GI:17397911  
Xenopus laevis  
African clawed frog.

REFERENCE  
AUTHORS  
TITLE

1 (bases 1 to 687)  
Kitayama, A., Terashima, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara, Y.  
Expressed genes in X. laevis embryo

JOURNAL Unpublished (2001)  
 COMMENT Contact: Tadasu Shin-i  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshini@genes.nig.ac.jp.

FEATURES  
 source  
 1. .687  
 /organism="Xenopus laevis"  
 /db\_xref="taxon:8355"  
 /clone="XL013e02"  
 /clone\_lib="NIBB Mochii normalized Xenopus neurula library"  
 /tissue\_type="whole embryo"  
 /dev\_stage="stage 15"  
 /notes="vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."

BASE COUNT 141 a 169 c 182 g 192 t 3 others  
 ORIGIN

Query Match 20.3%; Score 411.6; DB 13; Length 687;  
 Best Local Similarity 82.9%; Pred. No. 6.4e-78;  
 Matcheb 493; Conservative 0; Mismatches 100; Indels 2; Gaps 2;

Qy 563 CTAATTTGCCCCCAGCGTGAATCCACCCCGTCTTTGAAAACTGAAGCTGCTCACA 622  
 Db  
 686 CTCACGCTGCCCGGAAATGAGTCTCACCTGTGTAGAGAACTGAAGCGCCGCCACA 627  
 Qy 623 GCTACACCCG-AAAGAGTTTGAGTGAATCTGAAGCGGGCGTGTTCATCATCAAG 681  
 Db  
 626 GCTACACCCCGAAGGACTTTTGACTGGAACCTGAAATGAGCGTGTATTATATAAG 567  
 Qy 682 AGCTACTCTGAGGACGATCCACCGTCTCAATTAAGTACTCCATCTGCTGAGCACAGAG 741  
 Db  
 566 AGCTACTCTGAGGATGATATCCACCGTTCATCAATATCTCATCTGCTGAGCACAGAG 507  
 Qy 742 CACGGCAACAGCCGCTGGACAGCGCTTCGCTGCTATGACGACAGAGGGCCGCTCTAC 801  
 Db  
 506 CATGGGAATAACGCTTGGATTAACGCTTTCGCTCCATGAAATGGCAAGGCGCGTCTAC 447  
 Qy 802 CTGCTCTTCAGCGTCAATGGGAGTGGCATTTTGTGGGTGGCGGAGATGAAGTCCCCC 861  
 Db  
 446 CTTCTGTACGCGTCAACGGCAGTGGACACTTTTGGCGCGTAGCGGAGATGAAGTCCCCC 387  
 Qy 862 GTGACTACGGCACAGTGGCGGGTCTGGTCTCAGGACCAAGTGGAGGGGAAGTTTGAT 921  
 Db  
 386 GTGACTATGGCACAGTGGCGGGTCTGGTCTCAGGACCAATGGAAGGCAAGTTTGAC 327  
 Qy 922 GTCAGTGGATTTTGTAGGATGTACCCAAATACAGCTCCCGGACATCAGGCTGGAG 981  
 Db  
 326 GTCAAGTGGCTCTTTGTCAAGGAGGTTCCCAACACAGCTGAGGACATCCGCTGGAG 267  
 Qy 982 AATAACGACACAAACCGGTACAAACTCCCGGACACCCAGGAGTGGCTTAGAAAAA 1041  
 Db  
 266 AATAACGACACAAACCGGTACAAACTCCCGGACACCGAGAGGTTGCCCTTAGAAAAA 207  
 Qy 1042 GCCAAGCAAGTGTGAAATATCAGTTCTCTACAGGACACAACTCCATCTTCGACGAC 1101  
 Db  
 206 GCAAACTGGTGTAAATCATTTGCCACTTACAGCACAGCACTCCATCTTTGATGAC 147  
 Qy 1102 TTGCTCACTACGAGAGCGCA-GAGGAGGAGAGTGTGGTGCACAGGAAACGCG 1155  
 Db  
 146 TTTTCTCATTACGAGAGCGCAGGAGAGGAGGTTGTGCCAAGGTAACGC 92

RESULT 55  
 BM745243  
 LOCUS

DEFINITION K-EST0019074 SSSNU484 Homo sapiens cDNA clone SSSNU484-16-F12 5', mRNA sequence.  
 ACCSSION BM745243  
 VERSION BM745243.1 GI:19066572  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 432)  
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.  
 TITLE 21C Frontier Korean EST Project 2001  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongseung@mail.kribb.re.kr  
 Plate: 16 row: F column: 12  
 High quality sequence stop: 432.

FEATURES  
 source  
 1. .432  
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 /db\_xref="taxon:9606"  
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 /tissue\_type="Stomach"  
 /cell\_type="Epithelial"  
 /cell\_line="SNU-484"  
 /lab\_host="top10r"  
 /notes="Organ: Stomach; Vector: pTZ19RP1; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was decapped with tobacco acid pyrophosphatase (TAP) and ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dr-tailed vector. The dr-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli top10r' by electroporation method."

BASE COUNT 99 a 142 c 116 g 75 t  
 ORIGIN

Query Match 20.3%; Score 411; DB 14; Length 432;  
 Best Local Similarity 100.0%; Pred. No. 9e-78;  
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 400 GCTCAGCTCTCCAGCACAGCCCCAGCTTTGGCTCAACCGCAGTATCAGAGCCCTCAG 459  
 Db  
 5 GCTCAGCTCTCCAGCACAGCCCCAGCTTTGGCTCAACCGCAGTATCAGAGCCCTCAG 64  
 Qy 460 CAGCCACCCAGACCCGCTGGTTGCCCGCCACGCAACAGAACCGCGCTTTGGCAGAGC 519  
 Db  
 65 CAGCCACCCAGACCCGCTGGTTGCCCGCCACGCAACAGAACCGCGCTTTGGCAGAGC 124  
 Qy 520 GGAGGGCTGGCAGCGATAGCAACTCTCCTGGAAACGCTCCAGCTTAATCTGCCCCCAGC 579  
 Db  
 125 GGAGGGCTGGCAGCGATAGCAACTCTCCTGGAAACGCTCCAGCTTAATCTGCCCCCAGC 184  
 Qy 580 GTCAATCCACCCCGCTCTTGAATAACTCAAGGCTCTCACAGCTACAAACCCGAAAGAG 639  
 Db  
 185 GTCAATCCACCCCGCTCTTGAATAACTCAAGGCTCTCACAGCTACAAACCCGAAAGAG 244  
 Qy 640 TTTGAGTGGAACTTGAAACCGCGGTGTTTCATCATCAAGAGCTACTCTGAGGAGCAG 699

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Db 245 TTTAGTGGATCTGAAGCGGGCGTGTTCATCATCAAGAGCTACTCTGAGGAGC 304
QY 700 ATCCACCGTCCATTAAGTACTCCATCTGGTGTAGCAGAGCAGCGCAACAGCGCTG 759
Db 305 ATCCACCGTCCATTAAGTACTCCATCTGGTGTAGCAGAGCAGCGCAACAGCGCTG 364
QY 760 GACAGCGCTTCGGCTGCATGACGACGAGGCGCGCTTACCTGCTCTTC 810
Db 365 GACAGCGCTTCGGCTGCATGACGACGAGGCGCGCTTACCTGCTCTTC 415

RESULT 56
LOCUS B0737180 916 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8148583 NICHD XGC Emb4 Xenopus laevis cDNA clone
IMAGE:5542099 5', mRNA sequence.
ACCESSION B0737180
VERSION B0737180.1 GI:21876077
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 916)
REFERENCE NC1-Cgap http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NC1-Cgap clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Plate: LLAM12240 row: n column: 20
High quality sequence stop: 615.

FEATURES
Location/Qualifiers
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/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:5542099"
/dev_stage="embryo, stage 31-32"
/lab_host="DH10B (phage-resistant)"
/note="Organ: whole embryo; Vector: pCMV-SPORT6; Site: 1;
NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 2.1 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC
) library."
BASE COUNT 255 a 250 c 226 g 183 t 2 others
ORIGIN
Query Match 20.1%; Score 407.6; DB 14; Length 916;
Best Local Similarity 75.3%; Pred. No. 4.5e-77;
Matches 561; Conservative 0; Mismatches 175; Indels 9; Gaps 4;

QY 400 GCTCAGCTCTCCAGCAGACGCGCCAGCTTTGGCTCAACCGCAGTATCAGAGCCCTCAG 459
Db 44 GCTCAGCTCTCCAGCAGTGTCTCAGCTCCATATCAAAATCCAGCGCCCTCAGCAGCCA 103
QY 460 CAGCCACCCAGACCGCTGGTGGCCAGCAGCAGACGCGGCTTGGCAGAGC 519
Db 104 CAGTCTCCAGAAATCGTTGGTGGCCAGGAATAGGAACGCTGTTACGCTCAGGCT 163
QY 520 GGAGGGGCTGGCAGCGATAGCACTCTCTCTGGAAACGCTCCAGCTTAATCTGCCCCCAGC 579
Db 164 GGAGGCCAGACCGG-----AACCTTTGGAGGAGTCCAGCTCATGCTGCCCTCGGA 217
QY 580 GTCGAATCCCAACCCCGCTCTTGTGAATACTGAAGGCTGCTCAGAGCTACAAACCCGAAAGAG 639

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Db 218 AACGAATCTCACCTTGTCTAGAGAACTGAAGCGCGTCCACAGCTACAAACCCAGGAC 277
QY 640 TTTAGTGGAAATCTGAAAGCGCGCTGTGTTTCATCATCAAGAGCTACTCTGAGGAGCAGC 699
Db 278 TTTAGTGGAACTGAAGAAATGAAGCTGTGTTTATAATAAGAGCTATTCTGAGGATGAT 337
QY 700 ATCCACCGCTCCATTAAGTACTCCATCTGGTGTAGCAGAGCAGCGCAACAGCGCTG 759
Db 338 ATCCACCGTTCATCAATCAATCAATCTGTTGGTCAGCAGAGCATGGGAATAAACGCTG 397
QY 760 GACAGCGCTTCGGCTGCATGACGACGAGGCGCGCTTACCTGCTCTTCACGCTCAAT 819
Db 398 GATAGCGCTATTCGCTCCATGAATGAAGAAAGCGCGCTTACCTCTGTTACGCTCAAC 457
QY 820 GGAGTGGGCACTTTTGTGGGGTGGCGAGAGTGAAGTCCCCCGTGGAGTACGCGCACAGT 879
Db 458 GGCAGTGGACACTTCTGCGCGGTAGCCGAGATGAAGTCCCGTGGACTATGSCACAGT 517
QY 880 GCGGGGCTCGTCTCAGGACAAAGTGAAGGGAAGTTGATGTCCAGTGGATTTTGT 939
Db 518 GCAGGTGTCTGGTCAAGGACAAATGAAGGGAAGTGGAGTCAAGTGGCTCTTTGTC 577
QY 940 AAGGATGATCCCAATAAACAGCTCCGSCACAT-CAGGCTGGAGAAATAAGCAGCAACAAAC 998
Db 578 AAGAGCTTCCCAACAAACAGCTGAGGCAATNCCGCTGGAGAACAAACGACAAAC 637
QY 999 GGTCAACAACTCCCG-GGACACCCAGGAGTGCCTTTAGAAAAGGCAAGTGTCTGA 1057
Db 638 GGTCAACAACTCCCGAGAGACACGAGAGTGCCTTTAGAAAAGCAAACTGGTCTTA 697
QY 1058 AATATATCATGTTCTTACAGCACACAACTT-CATCTTCGACGACTTTGCTCTACTAGAG 1116
Db 698 AATCATTTGCCATTACAAGCACACGACCTCCCATCTTTGATGACTTTTCTCATTAGCAG 757
QY 1117 AAGCGCAGGAGGAGGAGTGGT 1141
Db 758 AAGCGCAGGAGGAGGAGTGGT 782

RESULT 57
LOCUS AV747364 548 bp mRNA linear EST 19-OCT-2000
DEFINITION AV747364 NPC Homo sapiens cDNA clone NPCBK10 5', mRNA sequence.
ACCESSION AV747364
VERSION AV747364.1 GI:10905212
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 548)
REFERENCE Qian, B., Liu, F., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Gu
, W., Tu, Y., Jia, J., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu
, Han, Z., Chen, Z., Hu, R. and Chen, J.
Homo sapiens NPC library cDNA clones
Unpublished (2000)
Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045(ex. 663332)
Fax: 86-21-64743206
Email: mbshi@ms.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.

FEATURES
Location/Qualifiers
1..548
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NPCBK10"

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/clone_lib="NPC"
/tissue_type="pituitary"
/dev_stage="Adult"
/lab_host="SOLR"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 149 a 118 c 127 g 143 t 11 others
ORIGIN

Query Match 20.0%; Score 406.6; DB 10; Length 548;
Best Local Similarity 91.0%; Pred. No. 7.7e-77;
Matches 483; Conservative 0; Mismatches 42; Indels 6; Gaps 5;

QY 915 GTTTGATGTCAGTGGATTTTGTAAAGATGTACCCCAATACAGCTCCGGCACATCAG 974
DB 1 GGTGTGATGGGAGCCAGGCTTTCACAGGACACACCTCAGCAGGCCCCCGGATGACAG 60

QY 975 GCTGGAGATTAACGACAAACACCGGTGACAAATCCCGGACACCCAGAGGTGCCCTT 1034
DB 61 CCTGGAGATTAACGACAAACACCGGTGACAAATCCCGGACACCCAGAGGTGCCCTT 120

QY 1035 AGAAAAGCCAGCAGTCTGCAAAATATCAGTTCTTACAGCAGACACCACTCCATCTT 1094
DB 121 AGAAAAGCCAGCAGTCTGCAAAATATCAGTTCTTACAGCAGACACCACTCCATCTT 180

QY 1095 CGAGCACTTTGCTCAGTACGAGAGGCGCA - GAGGAGGAGGAGGTGGTCCGCAAGGAACG 1153
DB 181 CGAGCACTTTGCTCAGTACGAGAGGCGCAAGGAGGAGGAGGTGGTCCGCAAGGAACG 240

QY 1154 GCAGAGTCGAAACAAACAAATCAGGCGGCAACAGTTTCTTACATGTTCTTAAGCTT 1213
DB 241 GNAAGTCNAAACAAACAAATCAGGCGGCAACAGTTTCTTACATGTTCTTAAGCTT 300

QY 1214 TGAACACAGTTTAAACACAGTGTGCTTGGTCACTCCAGTGTGCTCCCGGGGGT 1273
DB 301 TGAACACAGTTTAAACACAGTGTGCTTGGTCACTCCAGTGTGCTCCCGGGGGT 359

QY 1274 TGAGTGTGCACTTTGCTTCTTCTGCTTCTGCTTTGCTTCTGCTTCTGCTTCTGCTT 1333
DB 360 TGAGTGTGCACTTTGCTTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT 418

QY 1334 TTGTACTTTTCTATGATTAATAATCCTGTAGAGTCACTAATAAGGAGTATTTTTTT 1393
DB 419 TTGTACTTTTCTATGATTAATAATCCTGTAGAGTCACTAATAAGGAGTATTTTTTT 477

QY 1394 TGTGAGCTTATCAATCAGACTGATCTAATGTGAATGTGAATGTGAATGTGAATGTGA 1444
DB 478 --GCAGCTTATCAATCAGACTGATCTAATGTGAATGTGAATGTGAATGTGAATGTGA 526

RESULT 58
AL550164
LOCUS AL550164 LTI_NFL006.P12 Homo sapiens cDNA clone CS0DI040YK06 5
DEFINITION prime, mRNA sequence.
ACCESSION AL550164
VERSION AL550164.1 GI:12989688
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .1053
/organism="Homo sapiens"

FEATURES
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/db_xref="taxon:9606"
/clone="CS0DI040YK06"
/clone_lib="LTI_NFL006.P12"
/tissue_type="pituitary"
/notes="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 198 a 349 c 314 g 191 t 1 others
ORIGIN

Query Match 20.0%; Score 405.8; DB 9; Length 1053;
Best Local Similarity 98.3%; Pred. No. 1.1e-76;
Matches 410; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAAAAGCAGGATTAATAAGTACAAATGCTTCGTACATCAGAGGATACAGTTTCATG 60
DB 366 CAAAAGCAGGATTAATAAGTACAAATGCTTCGTACATCAGAGGATACAGTTTCATG 425

QY 61 ACAATGACTTTAGCCCTTACCTTACTGAGCAGTCAAAATCAGAGTAACAGTTTACCCCTCA 120
DB 426 ACAATGACTTTAGCCCTTACCTTACTGAGCAGTCAAAATCAGAGTAACAGTTTACCCCTCA 485

QY 121 TGACGACCCCTACCTGTCAGCTATTACCGCGCTCCATTTGGATTTCTTACTCCCTCA 180
DB 486 TGACGACCCCTACCTGTCAGCTATTACCGCGCTCCATTTGGATTTCTTACTCCCTCA 545

QY 181 ATGAGCTCGTGTGCTTACTGCGGAGCCCTCGATTCATACCTCACACCTACCGGAC 240
DB 546 ATGAGCTCGTGTGCTTACTGCGGAGCCCTCGATTCATACCTCACACCTACCGGAC 605

QY 241 AGCTCAGTAACGAGACATCATTTATGACAGTGTGCTTTTGGGAGCGCTGGGGGCC 300
DB 606 AGCTCAGTAACGAGACATCATTTATGACAGTGTGCTTTTGGGAGCGCTGGGGGCC 665

QY 301 TGGGAAACAACATCTATCAGCAGGTTCAATTTTTTCCCTGAAAAACCTGCGTTCTCAG 360
DB 666 TGGGAAACAACATCTATCAGCAGGTTCAATTTTTTCCCTGAAAAACCTGCGTTCTCAG 725

QY 361 CATGGGGAGCAAGTGGGCTCAGAGTCAGACGCCAGCTCAGCTCCCGACCA 417
DB 726 CATGGGGAGCAAGTGGGCTCAGAGTCAGACGCCAGCTCAGCTCCCGACCA 782

RESULT 59
AL514504
LOCUS AL514504 LTI_NFL006.P12 Homo sapiens cDNA clone CL0BB003ZF07 5
DEFINITION prime, mRNA sequence.
ACCESSION AL514504
VERSION AL514504.1 GI:12777998
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .977
/organism="Homo sapiens"

FEATURES
source
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Matches 537; Conservative 0; Mismatches 112; Indels 18; Gaps 5;

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Qy 787 AAGGGGCGCTACCTGCTCTTACGCTCAATGGAGTGGGCAATTTTGTGGGTGGCC 846
Db 5 AGGGGCGCGTTTATCTCTCTCAAGTGTCAATGGAGTGGGCAATTTTGTGGGTGGCA 64
Qy 847 GAGATGAATCCCCCGTGGACTACGGCACCAAGTCCCGGGTCTGGTCTCAGACAAAGTGG 906
Db 65 GAGATAAAGTCCCCGTGGATTACGGCACCAAGTCCCGGGTCTGGTCTCAGACAAAGTGG 124
Qy 907 AAGGGGAAGTTTGATGTCCAGTGGATTTTGTGAAGGATGTACCAATTAACAGCTCCGG 966
Db 125 AAGGGGAAGTTTGATGTGAAGTGGATTTTGTGAAGGATGTCCCAACCAACAGCTCCGG 184
Qy 967 CACATCAGGCTGGAGATAACGACAAACAAACCGGTTCACAACTCCCGGACACCCAGAG 1026
Db 185 CACATCAGACTGGAGATAACGACAAACAAACCTGTCAAACTCCCGGTGATACACAGAG 244
Qy 1027 GTGCCCTTAGAAAAAGCCAAAGTGTGAAATTTATCAGTTCTTACAAACACACACACC 1086
Db 245 GTGCCCTTAGAAAAAGCCAAACAAAGTGTGAAATTTATCGCTTCTTAAAGCACACACACC 304
Qy 1087 TCCATCTTCGACGACTTTGCTCACTACGAGAGCGCCA-GAGGAGGAGGAGTGTGGCG 1145
Db 305 TCTATCTTTGACGACTTTTCTATATGAGAGCGCCAGGAGGAGGAGTGTGGCGT 364
Qy 1146 AAGAAAGCGCAGATCGGAAACAAACAAATAGAGGGGAAACAGTCTTTTACATGTTTAAACG 1205
Db 365 AAGAAAGCAGAGATCGGAAACAAACAAATAGAGGAGTGTGTTGTTTGTGTTTAAATGGT 424
Qy 1206 TTTGACTTTGAAACAGTTTAAACACAGTGTGTTTGTGTCAGCT-----CCAGTG 1254
Db 425 TGACTTTGAAACAGAGTTTAAAGCTGTATGCTTGTGTGTCTCCGAGTCAGTCCAG 484
Qy 1255 TGTGCTCGCGCGCGGGTTCAGTGTGTCATCTTTCCTTTCCTGCTGCTGATTTTGGC 1314
Db 485 TGTGCTCTCGTGGGGTGTGATTTGTCATCTTTATCTTTTGTAG----TTCATTTTGC 540
Qy 1315 CAGATGATCTGCATTTTATTTGTACTTTTTCTATGATTAATAATCCTGTAGAGTCACTA 1374
Db 541 CAGATGATCTGCATCTTATTGTA-TTTTCTATGATTAATAATTTAGACTCACTA 599
Qy 1375 ATAAGGAGTATTTTGTGCTAGCTTATCAATCAGACTGATCTAATGTAATGTAAG 1434
Db 600 ATAAGGAGTATTTTGTGCTAGCTTATCAGTCACTTATGACCTAATGCAAAATATAA 658
Qy 1435 TATCCTT 1441
Db 659 TATCCTT 665
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RESULT 61
AW138532/c
LOCUS
DEFINITION UI-H-BII-abx-d-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2713371 3', mRNA sequence.
ACCESSION AW138532
VERSION AW138532.1 GI:6142850
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 441)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
The sequence contained an oligo-dr track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore may represent a bonafide poly A
```

tail. cDNA Library Preparation: M.B. Soares Lab Clone Distribution:  
NCI-CGAP clone distribution information can be found through the  
I.M.A.G.E. Consortium/LNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
Seq primer: M13 Forward  
POLYA=Yes.

#### FEATURES

source  
1..441  
/location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2713371"  
/clone\_lib="NCI\_CGAP\_Sub3"  
/lab\_host="DH10B (Life Technologies)"  
/notes="vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not 1; Site 2: Eco RI; The  
NCI CGAP Sub3 library is a subtracted library derived from  
the NCI CGAP Sub1 library, which is a subtracted library  
derived from B1. B1 constitutes a mixture of 21  
normalized or subtracted NCI CGAP libraries: NCI\_CGAP\_Co4  
, NCI\_CGAP\_Pr22, NCI\_CGAP\_Pr28, NCI\_CGAP\_Co10,  
NCI\_CGAP\_Co16, NCI\_CGAP\_Kid5, NCI\_CGAP\_Kid12,  
NCI\_CGAP\_Kid3, NCI\_CGAP\_Kid11, NCI\_CGAP\_Lym2,  
NCI\_CGAP\_Br2, NCI\_CGAP\_Co8, NCI\_CGAP\_CLL1, NCI\_CGAP\_Le12,  
NCI\_CGAP\_Brn23, NCI\_CGAP\_Lu5, NCI\_CGAP\_Lu24,  
NCI\_CGAP\_Lu19, NCI\_CGAP\_Gc4, NCI\_CGAP\_Gc6,  
NCI\_CGAP\_Brn25. These 21 libraries were pooled and a  
single-stranded DNA preparation of the resulting mixture  
was used as a tracer in a subtractive hybridization with  
a driver whose composition is detailed below:  
NCI\_CGAP\_Kid3 pool 1 LLAM 3334-3337, 3682-3683,  
3798-3803 (IMAGE CloneIDs 132376-1323911, 1456008-1456775  
, 1500552-1502855); NCI\_CGAP\_Kid5 pool 1 LLAM 3338-3342  
, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831,  
1471368-1472903, 1492104-1493255); NCI\_CGAP\_Lu5 pool 1  
LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991,  
1520904-1522439); NCI\_CGAP\_Gc4 pool 1 LLAM 3164-3167,  
3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,  
1469064-1470983, 1475592-1476743); NCI\_CGAP\_Pr22 pool 1  
LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs  
985608-986759, 1101192-1101959, 1217928-1220615);  
NCI\_CGAP\_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE  
CloneIDs 1057416-1061255, 1144584-1145351). Subtraction  
was performed as previously described (Bonaldi, Lennon &  
Soares (1996): Normalization and Subtraction: Two  
Approaches To Facilitate Gene Discovery. Genome Research  
6, 791-806.

TAG LIB=NCI\_CGAP\_Lu5  
TAG TISSUE=Lung  
TAG\_SEQ=CAAC"

BASE COUNT 117 a 100 c 93 g 131 t  
ORIGIN

Query Match 19.6%; Score 397.6; DB 10; Length 441;  
Best Local Similarity 98.8%; Pred. No. 6.7e-75;  
Matches 411; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
Qy 979 GAGAATAACGACACAAACCGGTTCACAAACTCCCGGACACCCAGGAGTCCCTTAA 1038  
Db 441 GAGAATAACGACACAAACCGGTTCACAAACTCCCGGACACCCAGGAGTCCCTTAA 382  
Qy 1039 AAGCCCAAGCAAGTCTGAAATTTATCAGTTCTTACAGACACACAACTCCATCTTC 1098  
Db 381 AAGCCCAAGCAAGTCTGAAATTTATCAGTTCTTACAGACACACAACTCCATCTTC 322  
Qy 1099 GACTTTCTCTACACGAGAGCGCCA-GAGGAGGAGGAGTGTGGCGCAGGAGGAGG 1157  
Db 321 GACTTTCTCTACACGAGAGCGCCA-GAGGAGGAGGAGTGTGGCGCAGGAGGAGG 262  
Qy 1158 AGTCGAAACAAACAAATGAGGCGCAACAGTTTCTTACATGTTCTTAACGTTTGA 1217  
Db 261 CGTCGAAACAAACAAATGAGGCGCAACAGTTTCTTACATGTTCTTAACGTTTGA 202  
Qy 1218 AACAGTTTAAACACAGTGTGCTTGGTCCAGTCCAGTGTGTCGTCCTCCGCGGGGTTG 1277

Db 201 AACAGTTTAAACACGTTGCTTGGTCAGCTCCAGTGTGTCGTCCTGGGGGTTGAG 142  
Qy 1278 TGTGTGATCTTTGCTTCTGTTGCTTGAATTTTGGCCAGATGGATCTGCAATTTATTTGT 1337  
Db 141 TGTGTGATCTTTGCTTCTGTTGCTTGAATTTTGGCCAGATGGATCTGCAATTTATTTGT 82  
Qy 1338 ACTTTTCTATGATTATATAATCTGTAGAGTCACTAATAAGAGGATTTATTTT 1393  
Db 81 ACTTTTCTATGATTATATAATCTGTAGAGTCACTAATAAGAGGATTTATTTT 26

RESULT 62  
AL526609  
LOCUS  
DEFINITION AL526609 LTI\_NFL003\_NBC3 Homo sapiens cDNA clone CS0DC020Y104 5 prime, mRNA sequence.  
ACCESSION AL526609  
VERSION AL526609.1 GI:12790102  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 826)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
source  
1..826  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0DC020Y104"  
/clone\_lib="LTI\_NFL003\_NBC3"  
/sex="male"  
/tissue type="neuroblastoma cells"  
/lab\_host="DH10B"  
/notes="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Peng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 168 a 270 c 239 g 147 t 2 others  
ORIGIN

Query Match 19.5%; Score 396.4; DB 9; Length 826;  
Best Local Similarity 98.3%; Pred. No. 1.1e-74;  
Matches 411; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 1 CAAGAAGACAGATATAAAGTACAAATGGTTGTTACATCAGAGATACAGTTTCATG 60  
Db 270 CAAGAAGACAGATATAAAGTACAAATGGTTGTTACATCAGAGATACAGTTTCATG 329

Qy 61 ACAATGACTTTGAGCCCTACTCTTACTCGACATCAATATCAGATTAACCTTCA 120  
Db 330 ACAATGACTTTGAGCCCTACTCTTACTCGACATCAATATCAGATTAACCTTCA 389

Qy 121 TGAGCGACCCCTACTCTTCTCCAGCTATTACCGCGCTCATTTGGATTTCTTACTCCCTCA 180  
Db 390 TGAGCGACCCCTACTCTTCTCCAGCTATTACCGCGCTCATTTGGATTTCTTACTCCCTCA 449

Qy 181 ATGAGGCTCGGTGCTACTTCGAGGGACCCCTCGATTCATACCTCACACCTACGGAC 240  
Db 450 ATGAGGCTCGGTGCTACTTCGAGGGACCCCTCGATTCATACCTCACACCTACGGAC 509

Qy 241 AGCTCAGTAACGAGACCATCATTTTATCCAGATCTGTTTTTGGGAGCTGGGGGCC 300  
Db 510 AGCTCAGTAACGAGACCATCATTTTATGCAGATCTGTTTTTGGGAGCTGGGGGCC 569  
Qy 301 TGGGGAAACACAT-CTATCAGCACAGGTTCAATTTTTTCCCTGAAAACCTCGGTTCTCA 359  
Db 570 TGGGGAAACACATCTATCTATCAGCACAGGTTCAATTTTTTCCCTGAAAACCTCGGTTCTCA 629  
Qy 360 GCATGGGGGACAAAGTGGGTCTCAAGGTTCAGCAGACCCAGAGCTCAGCCTCTCCACGCA 417  
Db 630 GCATGGGGGACAAAGTGGGTCTCAAGGTTCAGCAGACCCAGAGCTCCGGGTATGGGACCA 687

RESULT 63  
AL656188  
LOCUS  
DEFINITION AL656188 XGC-neurula Silurana tropicalis cDNA clone TNeu035i07 5', mRNA sequence.  
ACCESSION AL656188  
VERSION AL656188.1 GI:17668416  
KEYWORDS EST.  
SOURCE western clawed frog.  
ORGANISM Silurana tropicalis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Silurana.  
REFERENCE 1 (bases 1 to 702)  
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.  
Sanger Xenopus tropicalis EST project 2001 (10\_2001)  
Unpublished (2001)  
Contact: Huckle E  
Sanger Centre  
Hinxton, Cambridgeshire, CB10 1SA, UK  
Email: trop@sanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS\_SEQUENCE\_ID: TNeu035i07.sp6  
Sequencing primer: SP6  
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.

FEATURES  
source  
1..702  
/organism="Silurana tropicalis"  
/db\_xref="taxon:8364"  
/clone="TNeu035i07"  
/clone\_lib="XGC-neurula"  
/dev\_stages="neurula"  
/lab\_host="Escherichia coli DH10B"  
/note="Vector: pCS107; Site\_1: EcoRI; Site\_2: NotI; cDNA was oligo dT primed from Sug of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end."

BASE COUNT 162 a 254 c 185 g 100 t 1 others  
ORIGIN

Query Match 19.3%; Score 390.6; DB 9; Length 702;  
Best Local Similarity 80.9%; Pred. No. 2e-73;  
Matches 469; Conservative 0; Mismatches 105; Indels 6; Gaps 1;

Qy 436 CAACCGCAGTATCAGAGCCCTCAGCAGCCACCCAGACCCGCTGGTTGCCCCACGGAAC 495  
Db 129 CCACCGCCCTCAGCAGCAGCCACGAGCCCTCAGAACCGCTGGGTGGCCCAACGGAAC 188

Qy 496 AGAAGCGCGGCTTTGGGACAGCGGGGCTGGGCGGATAGCACTCTCTGGAAC 555  
Db 189 AGAAGCGGCTTTACGGCCAGGGCGGAGCCCGGACG-----GGACCTCTGGGGGGG 242

Qy 556 GTCACGCTAAATTTCTGCCCCAGCGTCGAATCCACCCCTCTCTGAAAAAAGTGAAGGCT 615  
Db 243 GCTCAGTCTCACTCCGCCCTCTGGAAACGAGTCCACCCCTCTCTGGAGAACTGAAGGCC 302

Qy 616 GTCACAGCTACAAACCGGAAAGATTTGAGTGAATCTGAAAGCGGGCGCTGTTCATC 675



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Db 303 GCCCAGCTACACCCCAAGGACTTTGACTGGAACTTGAAACCGGGCGGTGTTCTATA 362
Qy 676 ATCAAGAGTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCCATCTGTTGTAGC 735
Db 363 ATAAAGACTACTCCGAGGACGACATCCACCGCTCCATCAAGTACTCCATCTGTTGACG 422
Qy 736 ACAGAGCAGGCAACAGCGCTTGACAGCGCTTCCGCTGCTGATGAGCAGCAAGGGGCC 795
Db 423 ACAGAGCAGGCAACAGCGCTTGATAGCGCTTCCGCTCCATGAACGGAAGGGCCCC 482
Qy 796 GTCTACCTCTCTTCAAGGCTCAATGGGAGTGGCATTTTGTGGGTGGCCGAGATGAAG 855
Db 483 GTCTACCTCTCTTCAAGGCTCAACGGCAGCGGACACTTCTGCGGGTGGCCGAGATGAAG 542
Qy 856 TCCCGCTGGACTACGGCACCAGTCCCGGGGTCTGGTCTCAGGACAACTGGAAGGGGAAG 915
Db 543 TCCCGCTGGACTACGGCACCAGTCCCGGGGTCTGGTCTCAGGACAACTGGAAGGGGAAG 602
Qy 916 TTTGATGTCAGTGAATTTTGTAAAGATGTACCCATTAACAGCTCCGCGCACATCAGG 975
Db 603 TTCGAGCTCAAGTGGCTCTTCTGTCNCAAGACGTTCCTCAACAAACAGCTGAGGCACATCCG 662
Qy 976 CTGAGATACGACCAACAAACCGGTCTCAAACTCCCGG 1015
Db 663 CTGAGATACGACCAACAAACCGGTCTCAAACTCGCGC 702

RESULT 64
AL524373
LOCUS AL524373 LTI_NFL003_NBC3 820 bp mRNA linear EST 13-FEB-2001
DEFINITION AL524373 prime, mRNA sequence.
ACCESSION AL524373
VERSION AL524373.1 GI:12787866
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1. (bases 1 to 820)
AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
location/Qualifiers
source 1..820
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC06YG03"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_types="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 152 a 242 c 242 g 153 t 31 others
ORIGIN
Query Match 19.3%; Score 390.6; DB 9; Length 820;
Best Local Similarity 92.3%; Pred. No. 2e-73;
Matches 385; Conservative 21; Mismatches 11; Indels 0; Gaps 0;

```

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Qy 1 CAAAGGCAAGATAATAAAGTCAAAATGTTCTGTATCATCAGAAAGTATCAGTTTCATG 60
Db 275 CAAAGGCAAGATAATAAAGTCAAAATGTTCTGTATCATCAGAAAGTATCAGTTTCATG 334
Qy 61 ACAATGACTTTGAGCCCTACCTTACTGACAGTCAATCAAGTAAACAGTTACCCCTCAA 120
Db 335 ACAATGATTTTGGCAGTACCTTWTGCGAGTAAATYAGAGTTACAGTTACCTCAA 394
Qy 121 TGAGCGACCCCTACTCTGTCAGCTATTACCGCGCTGCATTTGGATTTCTTACTCCCTCA 180
Db 395 TGAGCGACCCCTACTCTGTCAGCTATTACCGCGCTGCATTTGGATTTCTTACTCCCTCA 454
Qy 181 ATGAGGCTCCGTGTTCTACTGCGAGGACCTCCGATTTCATACCTACACCTACGAGAC 240
Db 455 ATGAGGCTCCGTGTTCTACTGCGAGGACCTCCGATTTCATACCTACACCTACGAGAC 514
Qy 241 AGCTCAGTAACGAGACCATCATTTTATGACAGTGTCTTTTGGGAGCGCTGGGGGCC 300
Db 515 AGCTCAGTTACGAGACCATCATTTTATGACAGTGTCTTTTGGGAGCGCTGGGGGCC 574
Qy 301 TGGGGAACAACATCTATCAGCACAGTTCATTTTCCCTGAAACCCCTGCGTTCTCAG 360
Db 575 TGGGGAACAACATCTATCAGCACAGTTCATTTTCCCTGAAACCCCTGCGTTCTCAG 634
Qy 361 CATGGGGCAAGTGGGTCTCAAGGTCAGAGACCCAGAGCTCAGCTCTCCAGCA 417
Db 635 CATGGGGCAAGTGGGTCTCAAGGTCAGAGACCCAGAGCTCAGCTCTCCAGCA 691

RESULT 65
AL558224
LOCUS AL558224 LTI_NFL008_TC2 773 bp mRNA linear EST 16-FEB-2001
DEFINITION AL558224 prime, mRNA sequence.
ACCESSION AL558224
VERSION AL558224.1 GI:12902542
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1. (bases 1 to 773)
AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
location/Qualifiers
source 1..773
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DJ001YF07"
/clone_lib="LTI_NFL008_TC2"
/sex="male"
/tissue_types="T cells from T cell leukemia"
/notes="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 154 a 260 c 219 g 139 t 1 others
ORIGIN
Query Match 19.0%; Score 385.4; DB 9; Length 773;
Best Local Similarity 98.1%; Pred. No. 2.6e-72;
Matches 411; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

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QY 1 CAAAGGACAAGATAATAAGTACAAATGGTTCGTTACATCAGAAAGGATACAGTTTCATG 60
Db 277 CAAAGGACAAGATAATAAGTACAAATGGTTCGTTACATCAGAAAGGATACAGTTTCATG 336
QY 61 ACATGACTTTGAGCCCTACCTTACTGAGCAGTCAATCAGAGTAAACCTCCCTCAA 120
Db 337 ACAATGACTTTGAGCCCTACCTTACTGAGCAGTCAATCAGAGTAAACCTCCCTCAA 396
QY 121 TGAGCAGCCCTACCTTACTGAGCAGTCAATCAGAGTAAACCTCCCTCAA 180
Db 397 TGAGCAGCCCTACCTTACTGAGCAGTCAATCAGAGTAAACCTCCCTCAA 456
QY 181 ATGAGGCTCGTGGTCTACTGAGGAGACCTCCGATTCATACCTACCTACCTACCTAC 239
Db 457 ATGAGGCTCGTGGTCTACTGAGGAGACCTCCGATTCATACCTACCTACCTACCTAC 516
QY 240 CAGCTCAGTAAACGAGACCATATTTATGACGAGTCTGTTTGGGAGCCTGGGGGC 299
Db 517 CAGCTCAGTAAACGAGACCATATTTATGACGAGTCTGTTTGGGAGCCTGGGGGC 576
QY 300 CTGGGGAACAACATCTATCAGCAGAGTTCATATTTTCCCTGAAAACCTCGGTTCTCA 359
Db 577 CTGGGGAACAACATCTATCAGCAGAGTTCATATTTTCCCTGAAAACCTCGGTTCTCA 636
QY 360 GCAT-GGGGACAAAGTGGGTCTCAAGGTACAGCAGACCCAGAGCTCAGCCCTCTCCACGA 417
Db 637 GCATGGGGGACAAAGTGGGTCTCAAGGTACAGCAGACCCAGAGCTCAGCCCTCTCCACGA 695

RESULT 66
AL580105/c 772 bp mRNA linear EST 16-FEB-2001
LOCUS AL580105 LTI_NFL008_Tc2 Homo sapiens cDNA clone CSODJ001YF07 3
DEFINITION Prime, mRNA sequence.
ACCESSION AL580105
VERSION AL580105.1 GI:12945803
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1..772
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODJ001YF07"
/clone_lib="LTI_NFL008_Tc2"
/sex="male"
/tissue_type="T cells from T cell leukemia"
/notes="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 275 a 168 c 148 g 176 t 5 others
ORIGIN
Query Match 19.0%; Score 384.4; DB 9; Length 772;
Best Local Similarity 98.3%; Pred. No. 4.3e-72;

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Matches 395; Conservative 4; Mismatches 1; Indels 2; Gaps 1;
QY 1627 TTTTGTTCATTCTGATTTGTCATTTTATCTGTTATCGGTCTAAAGTGTCTAATTTTAC 1686
Db 772 TTTTGTTCATTCTGATTTGTCATTTTATCTGTTATCGGTCTAAAGTGTCTAATTTTAC 713
QY 1687 CAAATTTGATTTTCTGCTAGACAGATAACTTTTAAATTTTCAAAATTTGGCAGACACTTTT 1746
Db 712 CCAATTTGATTTTCTGCTAGACAGATAACTTTTAAATTTTCAAAATTTGGCAGACACTTTT 653
QY 1747 TTTTGTTCATTCTGATTTGTCATTTTATCTGTTATCGGTCTAAAGTGTCTAATTTTAC 1806
Db 652 TTTTGTTCATTCTGATTTGTCATTTTATCTGTTATCGGTCTAAAGTGTCTAATTTTAC 595
QY 1807 TCATGTCCTGTCGTCGATTCGGGCTGGATGCTGTTGGGSCATGATGTGTGAGGAACGTG 1866
Db 594 TCATGTCCTGTCGTCGATTCGGGCTGGATGCTGTTGGGSCATGATGTGTGAGGAACGTG 535
QY 1867 GAAGGTGCTTTAGGCTGCTGTTTCCAGGTCGGGCACTCTTTGTTGTTGCACATCTTTTAA 1926
Db 534 GAAGGTGCTTTAGGCTGCTGTTTCCAGGTCGGGCACTCTTTGTTGTTGCACATCTTTTAA 475
QY 1927 ATTTTACACCTTTTCTTAAGAATTTCTAATGCCGTCTTAAGTTTATACCAATAATGCTG 1986
Db 474 ATTTTACACCTTTTCTTAAGAATTTCTAATGCCGTCTTAAGTTTATACCAATAATGCTG 415
QY 1987 AGCTTTAAGTGTAGGATCTGCTAGTACAGACAGATGTGATGGA 2028
Db 414 AGCTTTAAGTGTAGGATCTGCTAGTACAGACAGATGTGATGGA 373

RESULT 67
B1283897/c 649 bp mRNA linear EST 19-JUL-2001
LOCUS B1283897 UI-R-CX0s-ccx-h-11-0-UI-s1 UI-R-CX0s Rattus norvegicus cDNA clone
DEFINITION UI-R-CX0s-ccx-h-11-0-UI 3', mRNA sequence.
ACCESSION B1283897
VERSION B1283897.1 GI:14936090
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
TITLE Rattus.
JOURNAL 1 (bases 1 to 649)
MEDLINE Bonaldo, M.P., Lennon, G. and Soares, M.B.
COMMENT Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
non-normalized rat placenta pool library cDNA Library Preparation:
M.B. Soares Lab Clone distribution: clones will be available
through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
Location/Qualifiers
1..649
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CX0s-ccx-h-11-0-UI"

FEATURES
source
1..649
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CX0s-ccx-h-11-0-UI"

```

```

/clone_lib="UI-R-CX0s"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: p7T3b-Pac (Pharmacia) with a modified
polylinker; Site_1: Not 1; Site_2: Eco RI; The UI-R-CX0s
library is a non-normalized library constructed from the
following rat placenta tissues: embryonic day 17,
embryonic day 19, embryonic day 21. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldi, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=UI-R-CX0s
TAG_TISSUE=rat placenta pool
TAG_SEQ=TCACGACGT"

```

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BASE COUNT      180 a   162 c   120 g   187 t
ORIGIN

Query Match      18.9%; Score 383.8; DB 13; Length 649;
Best Local Similarity 80.9%; Pred. No. 5.9e-72;
Matches 514; Conservative 0; Mismatches 102; Indels 19; Gaps 5;

```

```

Qy 771 CCGCTGCATGACGACGAAGGCGCGTCTACCTGCTCTTACGCGTCAATGGAGTGGGCA 830
Db 649 CCGCTCCATGACGACGAAGG--CCTGTTATTGCTCTTCAATGGAGTGGGCA 592

Qy 831 TTTTGTGGGTGGCGAGATGAAGTCCCGTGGACTACGGCACCGTGC CGGGGTCTG 890
Db 591 TTTCTGTGGGTGGCGAAGATGAAGTCCCGTGGACTACGGCACCGTGC TGGGGTCTG 532

Qy 891 GTCTCAGACCAAGTGGAGGGAGTTTGATGTCTCAGTGGATTTTTGTAAAGGATGTACC 950
Db 531 GTCTCAGACCAAGTGGAGGGAGTTTGATGTGAAGTGGATTTTGTCAAGGATGTCCC 472

Qy 951 CAATAACAGCTCCGGCAGCATCAGCTGGAGTAATACGACAAACACCGGTTCACAACTC 1010
Db 471 CAATAATCAACTGGCGCAGCATCAGCTGGAGTAATACGACAAACACCGCTGTCAAACTC 412

Qy 1011 CCGGACACCCAGAGGTGCCCTTAGAAAAAGCCAGCAAGTGTGTAATATTCAGTTTC 1070
Db 411 CCGTGACACCGAGGAGTGGCCCTTAGAAAAAGCCAGCAAGTGTGTAATATTCAGTTTC 352

Qy 1071 CTACAAGCACCAACCTCCATCTTCGACGACTTTGCTCACTACGAGAGCGCCCA-GAGGA 1129
Db 351 CTATAAGCACCAACCTCCATCTTCGACGACTTTTCTCATTTATGAGAGCGCCAGGAGA 292

Qy 1130 GGAGAGGTGTGGCAAGGAACGCGAGCTCGAACAACAATGAGAGGCGCAACGAGTTT 1189
Db 291 AGAGGAGGTAGTGGCAAGGAAGGAGCAATCGAACAACAATGAGAGGCGCGGTTT 232

Qy 1190 CTTACATGTTCTAACGTTTGACTTTGAAACAGATTTTAAACACAGTGTCTTGTCAGCT- 1248
Db 231 GTTTTGTGTTAATGGTTGACTTTGAAACAGAGTTTAAAGCTGTATGCTTGGTCTGTC 172

Qy 1249 -----CGAGTGTGTCGTCGCGCGGGTTCAGTGTTCATCTTTGCGCTTTCTT 1298
Db 171 TCCGAGTCAGCTCCAGTGTGTCGTCGCGGGTAAATGTCGATCTTTATCTTTGTA 112

Qy 1299 GTCGTTGATTTTTCGCCAGATGGATCTGCATTTATTTGATCTTTTCTATGATATAAT 1358
Db 111 G----TTCAATTTTTCGCCAGATGGATCTGCATTTCAATTTGTA-TTTTCTATGATATAAT 57

Qy 1359 CCTGTAGAAGTCACTAATAAAGGAGTATTTT 1393
Db 56 ATTGTAGAAGTCACTAATAAAGGAGTATTTTGT 22

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RESULT 68
BI662159      862 bp      mRNA      linear      EST 12-SEP-2001
LOCUS        603305178F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5350818 5',
DEFINITION   mRNA sequence.

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ACCESSION
VERSION      BI662159.1
KEYWORDS     house mouse.
SOURCE       Mus musculus
ORGANISM

```

```

REFERENCE
1 (bases 1 to 862)

```

```

AUTHORS      NTH-MGC http://mgc.nci.nih.gov/
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
              Ph.D.

```

```

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLNL at:
http://image.llnl.gov
Plate: LIAH11891 ROW: 1 column: 19
High quality sequence stop: 861.

```

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FEATURES
Source

```

```

1..862
   /organism="Mus musculus"
   /strain="NMRI"
   /db_xref="taxon:10090"
   /clone="IMAGE:5350818"
   /clone_lib="NCI_CGAP_Mam4"
   /tissue_type="tumor, gross tissue"
   /dev_stage="5 months"
   /lab_host="DH10B"

```

```

Note: Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996).

```

```

BASE COUNT      249 a   167 c   177 g   269 t
ORIGIN

```

```

Query Match      18.5%; Score 374.4; DB 13; Length 862;
Best Local Similarity 74.1%; Pred. No. 5.9e-70;
Matches 562; Conservative 0; Mismatches 171; Indels 25; Gaps 6;

```

```

Qy 844 GCCGAGATGAAGTCCCGTGGACTACGGCACCAAGTCCGGGTCTGCTCAGACCAAG 903
Db 1 GCAGAGATGAAGTCCCGTGGACTACGGCACCAAGTCCGGGTCTGCTCAGACCAAG 60

Qy 904 TGGAGGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGATGTACCAATTAACGAGTC 963
Db 61 TGGAGGGGAAGTTTGATGTGAAGTGGATTTTGTGAAGATGTGCCCAACCAACAGCTG 120

Qy 964 CGGCACATCAGGCTGGAGAATAACGACAAACACCGGTCTCAAACTCCCGGAGACCCAG 1023
Db 121 CGGCACATCAGCTGGAGATAACGACAAACACCTGTCAAACTCCCGTATACACAG 180

Qy 1024 GAGTGCCCTTAGAAAAAGCCAGCAAGTGTGAAATATTCAGTCTCTTCAACACACA 1083
Db 181 GAGTGCCCTTAGAAAAAGCAAAACAAAGTGTGGAAGATTTATCGCTTCTATAAGCACACA 240

Qy 1084 ACCTCCATCTTCGACGACTTTGCTCACTACGAGAGGCCCA-GAGGAGGAGGAGTGCTG 1142
Db 241 ACCTCTATCTTTGACGACTTTTCTCATTTATGAGAGGCCCAAGGAGGAGGAGTGCTG 300

Qy 1143 CGCAAGGAACGCGAGCTCGAAACAAACAATGAGGGCGCAACCACTTTTTCATGTTCTA 1202
Db 301 CGTAAGGAAGACAGAGATCGAAACAAACAATAAGAACCAAGCCAGTTTGTGTTGTTAAT 360

Qy 1203 ACGTTTGACTTTGAAACAGTTTAAACACAGTGTGCTGTGTCAGCT-----CCA 1251
Db 361 GGTTGACTTTGAAACAGAGTTTAAAGCTGTATGCTTGTGCTGTCTCCGAGTCAGCTC 420

```

double-stranded cDNA was ligated to a DraIII adaptor [GTGGCTACTG], digested and cloned into distinct DraIII sites of the pME18S-FU3 vector (5' site CACTGGG, 3' site CACCATGG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed and donated by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCCTGCTCAAAAGCTGG and 3' end primer

BASE COUNT	115 a	167 c	161 g	165 t
ORIGIN				

Query Match 17.9%; Score 363.8; DB 14; Length 608;  
Best Local Similarity 79.6%; Pred. No. 1.1e-67;  
Matches 442; Conservative 0; Mismatches 112; Indels 1;

604	AAACTGAAGGCTGCTCACAGCTACAACCCGAAAGAGTGTGGTGGAAATCTGAAAAGCGGG	663
Qy		
Db		
608	AAGCTCGTTCGGGCACACAGCTACAACCCCAAGGAGTTCGATTGGAACTCTGAAAATGGC	549
Qy		
664	CGTGTGTTTCAATCAAGAGCTACTCTGAGGACGACATCCAACGGCTCCATTAAAGTACTCC	723
Db		
548	CGGCTGTTTCAATCAATTAGAGCTACTCTGAGGACGAGCTCCATCGCTCCCATCAAGTACTCC	489
Qy		
724	ATCTGTGTAGCAGACAGACGACGCAACAAAGCGCTCGACAGCGCTTCCTCGTGCATGAGC	783
Db		
488	ATCTGTGTGAGACGAGAAATGGAACAAAGCGCTGGATTCTGCGTTTCTGCCATCAAC	429
Qy		
784	AGCAAGGGGCCCTCTACCTGTCTCTTACGGCTCAATGGGAGTGGGCAATTTTGTGGGGTG	843
Db		
428	GGCAAAAGTCTCTGTCTACCTGTCTGTTTACGCGTCAAACGGCAGCGGACACTTCTGTGGCGTG	369
Qy		
844	GCCGAGATGAAGTCCCCCGTGGACTACGGCACACAGTCCCGGGGTCTGGTCTCAGGACAAG	903
Db		
368	GCGGAGATGCGTTTCGCTGTGAGACTACGGCACAGTCCGCGTGTTTTGGGCGCAGGACAAG	309
Qy		
904	TGGNAGGGGAAGTTTCGATGTCACGTGGATTTTGTGTTAAAGATCTACCCAAATACCAAGCTC	963
Db		
308	TGGNAGGGGCAAAATTTGATGTGGACTGGCTGTTTTTTAAAGAGCTGCCCAACAGTCAAGCTC	249
Qy		
964	CGGCACATCAGGCTGGAGATAACGACAACAACCCGGTCAAACTCCCGGGACACCCAG	102
Db		
248	AGGCACATCCGCTGGAGACAATGACAACAAGCCCGTGACCAACTCGCGTGCACACAG	189
Qy		
1024	GAGGTGCCCTTAGAAAAGCCACGACGAGTCTGCAAAATTTATCAGTTCTCTACAGGCACA	108
Db		
188	GAGGTGCCCTCTGGAGAGGGCCACGACAGGTGCTCAAGATCATCTGCTACCTTACAAACACA	129
Qy		
1084	ACCTTCCATCTTCCAGCACTTTGCTACTACGAGAAGCGCCA-CAGGAGGAGGAGGTGGTG	114
Db		
128	ACCTTCCATCTTCCAGTACTTCTCACATTACGAGAAAGCGGACGAGGAGGAGAGGTGGTA	69
Qy		
1143	CGCAAGGAACGGCAG	1157
Db		
68	AGAAAGAACTCTTGAG	54

RESULT 70  
AW766504/C

AW/166504/C	LOCUS	AW766504	659 bp	mRNA	linear	EST 16-FEB-2001
	DEFINITION	da63dl1.x1 Harland stage 19-23 Xenopus laevis cDNA clone				
		IMAGE:3199605 3' similar to TR:064526 O64526 YUPH12R.13 PROTEIN.				
		.. mRNA sequence.				

ACCESSION AW766504  
VERSION AW766504.1 GI:7698494  
KEYWORDS EST.  
SOURCE African clawed frog.  
ORGANISM Xenopus laevis

ORGANISM  
Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
Xenopodinae; Xenopus.  
REFERENCE  
1 (bases 1 to 659)

Qy	1352	GTGRTCGTCCCGTGCGGGGGTTGAGTGTGCATCTTTTGCCCTTCCTTGTCGTCGTAATTTTT	1311
Dd	421	CAGTGTGCTCCTGTCGGGGTTGATTGTTGCACTTTATCTTTGTAG----TTCAATTTT	476
Qy	1312	GCCCAGATGGATCTGCATTTAATTTGTACTTTTTCTATGTAATATAAATCCTGTAGAAGTCA	1371
Dd	477	TGCCCAGATGGATCTGCATTTCAATTTGTGA-TTTTTCTGTATTATAAATTTGTAGAAGTCA	535
Qy	1372	CTAATAAAGGAGTATTTTTTTTCTGTCAGCTTATCAATCAGACGTCATCTAAATGTCAAAATGT	1431
Dd	536	CTAATAAAGGAGTA--TTCTGTTGTACGCTTATCAGTCAGATGGACCTAAATGCAANAATAT	593
Qy	1432	AAGTATCTCTAAAAACAAGCATCTAATTTGGCAGAAATGTGTTCCTTAAATTCAGTCAT	1491
Dd	594	AAATATTTCTCAAACAACAAACACCTAATACATCCAAGATAATTT-----TTATTITGG	647
Qy	1492	TTGATATTTCTGAGACTTCATAATTTCTCATCCCTTTATTCCTTTTTTAGCAAAACATAGA	1551
Dd	648	CAGAAATTAATGTTCTTATTTCTTATATCTAGCCATTTAATATCCCTATAGGATATTTTCATA	707
Qy	1552	AACCATGAGTCATTTTGTTCATTTTAGTAATTTCTGATAA	1589
Dd	708	TGCTTTTGCTCTCTCCTGCTTTTACAGCAACAAACAAA	745

RESULT 69

RESUB 69  
BM775261/C

[illegible]

BM775261  
ACCESSION

ACCESSION	BM775261	
VERSION	BM775261.1	GI:19104875

VERSION  
KEYWORDS  
EST.

KEYWORDS	SOURCE
EST.	zebrafish.

SOURCE	ORGANISM	LEGATION.
	Danio rerio	

Danio, Cyprinidae; Danio, Cyprinidae; Danio, Cyprinidae; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 608)  
; Cyprinidae; Danio.

1 (bases 1 to 508)

REFERENCE

AUTHORS

Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy  
S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood  
K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,  
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,  
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.  
and Wilson, B.

TITLE  
and Wilson, R.  
Washli Zebrafish EST Project 1998

TITLE	WashU Zebrafish ES	Unpublished (1998)
JOURNAL		

**JOURNAL COMMENT**  
Unpublished (1998)  
Contact: Stephen L. Johnson

**COMMENT**  
**Contact: Stephen L. Johnson**  
**Washington University School of Medicine**

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

4444 FOREL PARK  
Tel: 314 286 1800

**TEL: 314 286 1800**  
**Fax: 314 286 1810**

Fax: 314 288 1010  
Email: zbrafish@watson.wustl.edu

Endsara, Zsolt@lsbwa.dcu.hu, Rudi@lsbwa.dcu.hu  
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by Washington University Genome Sequencing Center Cloning and Distribution information can be found through the I.M.A.G.E. database.

distribution information can be found through the Consortium/LLNL, send email to: [info@image.llnl.gov](mailto:info@image.llnl.gov)

Seq primer: T7 from Gibco

seq primer: 1' from GIBCO  
High quality sequence stop: 472.

## FEATURES

source

1. .608

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1. 000
/organism="Danio rerio"
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/db_xref="taxon:7955"
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/clone="5602069"
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/clone_lib="Sugano SJD :
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/sex="male"
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/tissue_type="whole body"
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/dev_stage="adult"

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/lab_host="DH10B (phage resistant)"
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/note="Vector: pME18S-FL3; Site\_1: DraIII (CACCATGTG);

Site 2: DraIII (CACTGTGTG); 1st<sup>-</sup> strand cDNA was primed

## AUTHORS

Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.

## TITLE

WashU Xenopus EST project, 1999

## JOURNAL

Unpublished (1999)

## COMMENT

Other ESTs: da63d11.y1

Contact: Sandy Clifton, Ph.D.

WashU Xenopus EST project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Library constructed by R. Harland, PhD. (University of California, Berkeley)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml

Seq primer: -40UP from Gibco

High quality sequence stop: 503.

## FEATURES

source

1. .553

/organism="Xenopus laevis"

/db\_xref="taxon:8355"

/clones="IMAGE:3199605"

/clone\_lib="Harland stage 19-23"

/tissue\_type="neural"

/dev\_stage="stage 19-23"

/lab\_hosts="DH10B (phage-resistant)"

/note="vector: pCS107 (custom); Site 1: NotI; Site 2: SalI; cDNA made by oligo-dT priming. Library constructed by Dr. Francesca Mariani in the laboratory of R. Harland, Ph.D. (University of California, Berkeley). References:

XBP-2 is a transcriptional repressor that converts ectoderm into neural tissue. Mariani, F.V. Harland, R.M., Development. 1998 Dec;125(24):5019-31. PMID: 9811586; UI: 99030283; Use of large-scale expression cloning screens in the xenopus laevis tadpole to identify gene function.

Grammer TC, Liu KJ, Mariani FV, Harland RM. Dev Biol. 2000 Dec 15;228(2):197-210. PMID: 11112324; UI: 20564075; 2000 Dec 15;228(2):197-210. PMID: 11112324; UI: 20564075;

Note: This is a Xenopus Gene Collection (XGC) library."

BASE COUNT 148 a 161 c 153 g 196 t 1 others

## FEATURES

source

1. .733

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5115652"

/clone\_lib="NIH\_MGC\_12"

/tissue\_type="cervical carcinoma cell line"

/lab\_host="DH10B"

/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.4 kb. Library prepared by Life Technologies."

BASE COUNT 176 a 234 c 200 g 123 t

## BASE COUNT

ORIGIN

Query Match

Best Local Similarity 17.9%; Score 362.6; DB 13; Length 733;

Matches 390; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

Qy 400 GCTCAGGCTCTCCAGCACAGCCCCAGCTTTGGCTCAACCGCAGTATCAGAGCCCTCAG 459

Db 333 GCTCAGGCTCTCCAGCACAGCCCCAGCTTTGGCTCAACCGCAGTATCAGAGCCCTCAG 392

Qy 460 CAGCCACCCAGACCCCTGGTTGCCCGCCAGCAAGAACCGCGGGCTTTGGCGAGGC 519

Db 393 CAGCCACCCAGACCCCTGGTTGCCCGCCAGCAAGAACCGCGGGCTTTGGCGAGGC 452

Qy 520 GGAGGGCTGGCAGCGATAGCAACTCTCTGGAAACGTCAGCCTAATTTCTGCCCCGAGC 579

Db 453 GGAGGGCTGGCAGCGATAGCAACTCTCTGGAAACGTCAGCCTAATTTCTGCCCCGAGC 512

Qy 580 GTGGAATCCACCCCGCTCTTTGAAAAAAGCTGAAGGCTGCTCACAGCTACAAACCCGAAAGAG 639

Db 360 AAGTGGCTCTTTGTCAAGGAGCTTTCCCAACCAACCAAGCTGAGGCGACATCCCGCTGGAGAT 301

Qy 625 TACAACCCGAAAGAGTTTGAGTGGAAATCTGAAAGCGGGCGTGTGTTTCATCATCAAGAGC 684

Db 659 TATAACCTTAGGATTTTGAGTGGAAATCTGAAAGCGGGCGTGTGTTTCATCATCAAGAGT 600

Qy 685 TACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCCATCTCGGTGTAGCAGAGCAC 744

Db 599 TATT-TGAGGATGATATCCCGTTCATCATCATATTCATTCGTTGGTGCAGCAGAGCAT 541

Qy 745 GGCAACAGCGCTGGACAGCGCTTCGGTGCATGACGACAGGCGGCGCTTACTCTG 804

Db 540 GGGAAATAACCGCTGGATTAACCGCTTCGGTGCATGAAATGGCAAGGCGGCGCTTACTCT 481

Qy 805 CTCCTTACGCGTCAATGGGAGTGGGCGATTTTGTGGGGTGGCGGAGATGAAGTCCCGCGT 864

Db 480 CTGTTACGCGTCAACGCGAGTGGACATTTTTCGGCGTGGCGGAGATGAAGTCCCGCGT 421

Qy 865 GACTACGCGACCATGCGGGGGTCTGGTCTCAGGACAGTGGAGGGGAAAGTTTGTATGTC 924

Db 420 GACTATGGCACCACTGGCGGTGTCTGGTCTCAGGACAAATGGAAGGGCAAGTTTGACGTC 361

Qy 925 CAGTGGATTTTGTAGGATGTACCCCAATTAACCAAGCTCCCGCACATCAGGCTGAGNAT 984

Db 360 AAGTGGCTCTTTGTCAAGGAGCTTTCCCAACCAACCAAGCTGAGGCGACATCCCGCTGGAGAT 301

Qy 580 GTGGAATCCACCCCGCTCTTTGAAAAAAGCTGAAGGCTGCTCACAGCTACAAACCCGAAAGAG 639

Db 360 AAGTGGCTCTTTGTCAAGGAGCTTTCCCAACCAACCAAGCTGAGGCGACATCCCGCTGGAGAT 301

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Db 513 GTGGAATCCACCCCGTCTTGACAACTGAAGGCTGCCTCAGAGCTACCAACCCGAAAGAG 572
Qy 640 TTTGAGTGAATCTGAAAGCGGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGAC 699
Db 573 TTTGAGTGAATCTGAAAGCGGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGAC 632
Qy 700 ATCCACCGCTCCATTAAAGTACTCCATCTGCTGTAGCAGACGCGGCAACAGCCCTG 759
Db 633 ATCCACCGCTCCATTAAAGTACTCCATCTGCTGTAGCAGACGCGGCAACAGCCCTG 691
Qy 760 GACAGCGCTTCGCTGCATGACGACGAGGCGCCGCTCTA 800
Db 692 GACAG-GCCTTCGCTGCATGAGCGCAAGGGGCGCGCTCTA 731

RESULT 72
B542677
LOCUS B542677
DEFINITION B542677 790 bp mRNA linear EST 09-AUG-2000
ACCESSION B542677
VERSION B542677
KEYWORDS B542677.1 GI:9771322
SOURCE EST.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 790)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L14M8436 row: b column: 20
High quality sequence stop: 632.
Location/Qualifiers
1. .790
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3453235"
/clone_lib="NIH MGC 10"
/cell_line="WGC36"
/lab_host="DH10B"
/notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: Not I;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.5 Kb. Library prepared by Life
Technologies."
BASE COUNT 187 a 226 c 226 g 155 t
ORIGIN
Query Match 17.8%; Score 361.8; DB 10; Length 790;
Best Local Similarity 97.7%; Pred. No. 3e-67;
Matches 388; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

Qy 23 ACAAATGGTTGGTTACATCAGAGGATACAGTTTCATGACAAGTACTTTTCAGGCGCTACCT 82
Db 1 ACAAATGGTTGGTTACATCAGAGGATACAGTTTCATGACAAGTACTTTTCAGGCGCTACCT 60
Qy 83 TACTGGACAGTCAATCAGAGTAACTACCTTACCTCAATGAGCGACCCCTACCTGTCCAG 142
Db 61 TACTGGACAGTCAATCAGAGTAACTACCTTACCTCAATGAGCGACCCCTACCTGTCCAG 120
Qy 143 CTATTATCCCGCGTGCATTGGATTTCCTTACTCCCTCAATGAGGCTCCGTGGTCTACTGC 202
Db 121 CTATTATCCCGCGTGCATTGGATTTCCTTACTCCCTCAATGAGGCTCCGTGGTCTACTGC 180

```

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Qy 203 AGGGGACCCCTCCGATTCATACCTCACCACCTACGGA-CAGCTCAGTAAACGAGACCATC 261
Db 181 AGGGGACCCCTCCGATTCATACCTCACCACCTACGGA-CAGCTCAGTAAACGAGACCATC 240
Qy 262 ATTATTATG-CAGGATGCTGTTTTCGGGAGCCTGGGGGCTGGGGAACAACATCTATCAG 320
Db 241 ATTATTATGTCAGATGCTGTTTTCGGGAGCCTGGGGGCTGGGGAACAACATCTATCAG 300
Qy 321 CACAGGTTCAATTTTTTCCCTCAAAACCCCTGCGTTCTCAGCATGGGGGCAAAAGTGGGTCT 380
Db 301 CACAGGTTCAATTTTTTCCCTCAAAACCCCTGCGTTCTCAGCATGGGGGCAAAAGTGGGTCT 360
Qy 381 CAAGGTCAGCAGACCCAGAGCTCAGCCTTCCAGCA 417
Db 361 CAAGGTCAGCAGACCCAGAGCTCCGCGTATGGGAGCA 397

RESULT 73
B5025564/c
LOCUS B5025564
DEFINITION B5025564 674 bp mRNA linear EST 31-MAY-2002
ACCESSION B5025564
VERSION B5025564
KEYWORDS B5025564.1 GI:10755991
SOURCE EST.
ORGANISM African clawed frog.
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 674)
AUTHORS Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D.,
Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person,
B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
Waterston, R. and Wilson, R.
WASHU Xenopus EST project, 1999
Other ESTs: dg06d04.y1
Contact: Sandy Clifton, Ph.D.
WASHU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 458.
Location/Qualifiers
1. .674
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XENOPUS_SOURCE_ID:xlmgga002n08"
/clone_lib="Xenopus laevis gastrula non normalized"
/tissue_type="gastrula (stages 10.5, 11.5 mixed)"
/lab_host="Top-10 F"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from 2ug of poly A+ RNA (equal
parts from stage 10.5 and stage 11.5 gastrulae).
EcoRI-XhoI cut cDNA was then ligated into Unizap-XR
(Stratagene) with EcoRI at the 5' end and XhoI at the 3'
end. SS-library phagemids were prepared by mass excision
from the original library and normalized by hybridization
to biotinylated driver (prepared from the same library by
PCR) to Cot-omega of 11. After removal of hybrids and
excess driver by streptavidin sepharose chromatography,
the ss-phagemids were made double stranded and

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electroporated into Top-10 F'. Original library  
construction by Bruce Blumberg (Cho et al. 1991 Cell  
1111-1120). Note: This is a Xenopus Gene Collection (XGC)  
library."

BASE COUNT 139 a 169 c 169 g 197 t  
ORIGIN

Query Match 17.8%; Score 360.2; DB 12; Length 674;  
Best Local Similarity 79.4%; Pred. No. 6.7e-67;  
Matches 439; Conservative 0; Mismatches 113; Indels 1; Gaps 1;

QY 604 AAATGAGGCTGCTCAGCTACAACCCGAAAGAGTTGAGTGAATCTGAAAAGGGG 663  
DB 674 AATGTAGGGCCGCCCTACAGCTACAACCCCAAGGAGCTGTGATGAACCTCTAGAAATGAA 615  
QY 664 CGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCC 723  
DB 614 CGTGTGTTTAAATTAAGAGGCTACTCTGAGGATGATACCCCGTTCATCAATATCTCC 555  
QY 724 ATCTGGTGTAGCAGACGACGCGCAACAAAGCGCTGGACAGCGCTTCCGCTGCATGAGC 783  
DB 554 ATCTGGTGCAGCAGAGAGCTGGGAATAAACGCTTGGATAACGCTTCCGCTCCATGAAT 495  
QY 784 AGAAGGGGCCGCTTACCTCTCTTACGCTCAATGGAGTGGCATTTTGTGGGGTG 843  
DB 494 GCGAAGGGCCCGCTTACCTCTCTTACGCTCAACGCGTGGACACTTTTGGCGGCTA 435  
QY 844 GCCAGATGAATGCCCGTGGACTACGGCACAGTCCGGGGTCTGTCTCAGGACAA 903  
DB 434 GCCAGATGAATGCCCGTGGACTATGGCACAGTCCGGGTCTGTCTCAGGACAA 375  
QY 904 TGGAGGGGAGTTTGATGTCCAGTGGATTTTGTAAAGGATGTACCAATAACACAGCTC 963  
DB 374 TGGAGGGGCAAGTTTGAGCTCAAGTGGCTCTTGTCAAGGAGCTTCCCAACACAGCTG 315  
QY 964 CGGCACATCAGCTGGAGATAAAGCAACAAACCGGTCAAAACTCCCGGGACACCCAG 1023  
DB 314 AGGCACATCCGCTGGAGATAAAGCAACAAACCGGTCAAAACTCCCGGACACCCAG 255  
QY 1024 GAGTGCCCTTAGAAAAGCAACAGCTGCTGAAATATATCAGTTCTTACAAACACACA 1083  
DB 254 GAGTGCCCTTAGAAAAGCAAAACTGCTGCTTAAATCATTTGCCACTTACAGCACAG 195  
QY 1084 ACCTCCATCTTCGACGACTTTGCTCACTACGAGAGCGCCA-GAGGAGGAGGAGTGCTG 1142  
DB 194 ACCTCCATCTTTGATGACTTTTCTCATTCAGGAGCGGAGGAGAGAGGAGGTTGTG 135  
QY 1143 CGCAAGGAACGGC 1155  
DB 134 CGCAAGGTAACGC 122

RESULT 74  
BI713733  
LOCUS ie03d02.y1 HR85 islet Homo sapiens cDNA clone IMAGE:5086106 5',  
DEFINITION mRNA sequence.  
ACCESSION BI713733  
VERSION BI713733.1 GI:15689428  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 598)  
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,  
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,  
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,  
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas  
M., Gibbons,M., McCann,R., Cole,R., Teagareishvili,R., Williams,T.  
J., Jackson,Y. and Bowers,Y.  
Endocrine Pancreas Consortium  
Unpublished (2000)

COMMENT

Other\_ESTs: ie03d02.xl  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@biohp.harvard.edu  
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Dr. Hiroshi Inoue  
(hinoue@im.wustl.edu)  
Seq primer: -40RP from Gibco  
High quality sequence stop: 463.

FEATURES  
source

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/clone="IMAGE:5086106"  
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/tissue\_type="Purified pancreatic islet"  
/lab\_host="DH10B"  
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:  
NotI; Site\_2: XhoI; cDNA made by oligo-dT priming.  
Size-selected on agarose gel. Average insert size ~1kb. 5'  
XhoI site was destroyed after directional cloning.  
Amplified once. Contact information: Hiroshi Inoue, MD,  
Metabolism Div. (Alan Permutt Lab), Washington University  
School of Medicine, Box 8127, 660 South Euclid Ave., St.  
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
314-362-1916, Fax: 314-747-2692."

BASE COUNT 132 a 109 c 137 g 220 t  
ORIGIN

Query Match 17.6%; Score 356.8; DB 13; Length 598;  
Best Local Similarity 98.9%; Pred. No. 3.6e-66;  
Matches 370; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 1657 ATCTGTTATCGGTCTAAAGTGTCTAATTTACCCATTTCTGCTAGACAGATAACT 1716  
DB 8 ATCTGTTATCGGTCTAAAGTGTCTAATTTACCCATTTGATTTTCTGCTAGACATAACT 67  
QY 1717 TTTAAATTTTCAAATTTGGCAGACAC--TTTTTTTTTTTTTTTGAATACTTTCTTCCA 1774  
DB 68 TTTAAATTTTCAAATTTGGCAGACACATTTTTTTTTTTTTTTTGAATACTTTCTTCCA 127  
QY 1775 GATCTGTGCCCTACTGAACAGCCACCGTCTCCTCAGTCTGTCGCGATTGCGGCTGG 1834  
DB 128 GATCTGTGCCCTACTGAACAGCCACCGTCTCCTCAGTCTGTCGCGATTGCGGCTGG 187  
QY 1835 ATGCTGTGGGGCATGATGTGGAGGAACCTGGAAGTGTCTTAGGTCTGTTTCAGGCTC 1894  
DB 188 ATGCTGTGGGGCATGATGTGGAGGAACCTGGAAGTGTCTTAGGTCTGTTTCAGGCTC 247  
QY 1895 GGGCATTTCTTTGTTGTTGACATCTTTTAAATTTTACACCTTTTCTTAAGAAATTTCAA 1954  
DB 248 GGGTTTCTTTGTTGTTGACATCTTTTAAATTTTACACCTTTTCTTAAGAAATTTCAA 307  
QY 1955 TGCCGCTCTTAAGTTTATACCAATAATGCTGAGCTTTAAGTGTAGGATCTGGTAGTACA 2014  
DB 308 TGCCGCTCTTAAGTTTATACCAATAATGCTGAGCTTTAAGTGTAGGATCTGGTAGTACA 367  
QY 2015 GACAGTGTGATGGA 2028  
DB 368 GACAGTGTGATGGA 381

RESULT 75  
BM828295  
LOCUS BM828295  
DEFINITION K-EST0101085 S22SNUI6n1 Homo sapiens cDNA clone S22SNUI6n1-111-B10  
5', mRNA sequence.

BM828295 361 bp mRNA linear EST 06-MAR-2002  
LOCUS S22SNUI6n1 Homo sapiens cDNA clone S22SNUI6n1-111-B10  
5', mRNA sequence.

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ACCESSION   BM828295
VERSION     BM828295.1  GI:19184704
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 361)
AUTHORS    Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE      21C Frontier Korean EST Project 2001
JOURNAL     Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 111 row: B column: 10
            High quality sequence stop: 361.

FEATURES             Location/Qualifiers
     source           1..361
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="S22SNU16n1-111-B10"
                     /clone_lib="S22SNU16n1"
                     /sex="F"
                     /tissue_type="Ascites"
                     /cell_type="Lymphoblast-like"
                     /cell_line="SNU-16"
                     /lab_host="DH10B"
                     /note="Organ: Stomach; Vector: pT7T3-Pac; Site 1: EcoRI;
                     Site 2: NotI; The S22SNU16 library was contributed by the
                     Soares laboratory and it was constructed as described by the
                     Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
                     Research 6(9): 791-806. RNA was prepared from harvested
                     cells of SNU-16 culture. SNU-16 cell was obtained from
                     Korean Cell Line Bank (KCLB). SNU-16 was established from
                     ascitic fluids of Korean patients by Park J.G. et al.
                     (1990), Cancer Res 50: 2773-2780."
BASE COUNT   78 a 66 c 71 g 146 t
ORIGIN
Query Match      17.3%; Score 351.4; DB 14; Length 361;
Best Local Similarity 98.3%; Pred. No. 5.5e-65;
Matches 355; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1605 CTGAATCAAAAGGTTAATGATTTTGTTCATTCGATTTGTTCATTTATTTATCTGTTA 1664
DB 1 CTGAATCAAAAGGTTAATGATTTTGTTCATTCGATTTGTTCATTTATTTATCTGTTA 60

QY 1665 TCGGTCTAAAGTGCTAATTTACCATTTGATTTTTCGTAGACAGATACTTTTAATTT 1724
DB 61 TCGGTCTAAAGTGCTAATTTACCATTTGATTTTTCGTAGACAGATACTTTTAATTT 120

QY 1725 TTCAAATTTGGCAGACACTTTTTCATTTTTCGAAATCTTTCCTTCCAGATCTGTGC 1784
DB 121 TTCAAATTTGGCAGACACTTTTTCATTTTTCGAAATCTTTCCTTCCAGATCTGTGC 180

QY 1785 CCACCTGAACAGCCACCGCTCCCTCAGTGTCTGTGTCCGATTTGGGTGATGTTGG 1844
DB 181 CCACCTGAACAGCCACCGCTCCCTCAGTGTCTGTGTCCGATTTGGGTGATGTTGG 240

QY 1845 GGCATGATGTGTGGAGGAATCGGAAGTGCTTTTAGGTCTGGTTCAGGGTCGGGCACTTTT 1904
DB 241 GGCATGATGTGTGGAGGAATCGGAAGTGCTTTTAGGTCTGGTTCAAGGTCGGGCACTTTT 300

QY 1905 TGTGTTTGACATCTTTTAAATTTTACACCTTTTCTTAAGAAATCTTAATGCGGCTTTA 1964
DB 301 TGTGTTTGACATCTTTTAAATTTTACACCTTTTGGGTTTGAAGAAATCTTAATGCGGCTTTA 360

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QY 1965 A 1965
DB 361 A 361

RESULT 76
BE715628/c
LOCUS     BE715628
DEFINITION CM3-HT0745-150600-213-a04 HT0745 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE715628
VERSION   BE715628.1  GI:10103893
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 373)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE   20202663
COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=4t2=CM3-HT0745-150
            600-213-a04&t3=2000-06-15&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 14
            High quality sequence stop: 371.

FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone_lib="HT0745"
                     /dev_stage="Adult"
                     /note="Organ: head neck; Vector: puc18; Site_1: SmaI;
                     Site 2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT   83 a 109 c 92 g 89 t
ORIGIN
Query Match      17.3%; Score 350.8; DB 12; Length 373;
Best Local Similarity 99.2%; Pred. No. 7.4e-65;
Matches 363; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 626 ACAACCCGAAAGAGTTTGAGTGGAAATCTGAAAGCGGGGTGTGTTTCATCATCAAGAGCT 685
DB 372 ACAACCCGAAAGAGTTTGAGTGGAAATCTGAAAGCGGGGTGTGTTTCATCATCAAGAGCT 313

QY 686 ACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCCATCTGGTGTAGCAGAGACG 745
DB 312 ACTCTGAGGACGACATCCACCGCTCCATTAAGTACTCCATCTGGTGTAGCAGAGACG 253

QY 746 GCACCAAGCGCTGGACAGCGCTTCGGCTGCATGACGACGAGGGGCCGCTACTCTGC 805
DB 252 GCACCAAGCGCTGGACAGCGCTTCGGCTGCATGACGACGAGGGGCCGCTACTCTGC 193

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Db 477 AACTAGTAATGGAGACCATCACTTCATGCATGATGCTGTTTGGGAGCGCTGGGGTC 536
Qy 301 TGGGGAACAACATCTATCAGCAGCAGGTTCAATTTTCCCTGAAACCCCTCGGTTCTCAG 360
Db 537 TGGGGAACAACATTTACAGCAGCAGGTTTAATTTTCCCTGAAACCCCTCGATTCTCAG 596
Qy 361 CATGGGGACAAGTGGGTCTCAAGTTCAGCAGACCCAGAGCTCAGCCTCTCCACGCA 417
Db 597 CATGGGGACAAGTGGGTCTCAGGGGACAGACTCAGAGCTCAGCCTATGGGAGCA 653

RESULT 80
BQ927973 1041 bp mRNA linear EST 20-AUG-2002
LOCUS AGENCOURT 8861752 NCI CGAP Mam2 Mus musculus cDNA clone
DEFINITION IMAGE:6439636 5', mRNA sequence.
ACCESSION BQ927973
VERSION BQ927973.1 GI:22343004
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1041)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: csape@remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution by: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LIA3959 row: p column: 05
High quality sequence stop: 413.
Location/Qualifiers
1..1041
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/clone_lib="NCI CGAP Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 202 a 355 c 280 g 204 t
ORIGIN
Query Match 17.0%; Score 345; DB 14; Length 1041;
Best Local Similarity 89.2%; Pred. No. 1.2e-63;
Matches 372; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy 1 CAAAGGACAGATATAAAGTACAAATGGTTGTTACATCAGAGGATACAGTTTCATG 60
Db 28 CAAAGGACAGATATAAAGTACAAATGGTTGTTACATCAGAGGATACAGTTTCATG 87
Qy 61 ACAATGACTTTGAGCGCTTACTTGACAGAGTCAAAATCAGAGTAACAGTTACCCCTCAA 120
Db 88 ACAATGACTTTGAGCGCTTACTTGACAGAGTCAAAATCAGAGTAACAGTTACCCCTCAA 147
Qy 121 TGAGCGACCCCTACTCGTCCAGCTATTATACCGCGCGTCCGATTTGGAFTTCTCTTACTCCCTCA 180
Db 148 TGAGTGATCCCTTACTCGTCCAGTACTATACCAACATCCATTGGATTTCTTACTCCCTCA 207
Qy 181 ATGAGGCTCCGTGCTACTCGAGGGGACCCCTCCGATTCGATACCTACCAACCTACGGAC 240
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Db 208 GCGAGGACCATGGTCCACTGCAGGGGACCCCTCCCATCCGATCTCTCACTACCTATGAC 267
Qy 241 AGCTCAGTAACGGAGACCATCAATTTTATGACGATGCTGTTTTTGGGACAGCCTGGGGGCC 300
Db 268 AACTTAGTAATGGAGACCATCACTTCATGCATGATGCTGTTTTTGGGACAGCCTGGGGGTC 327
Qy 301 TGGGGAACAACATCTATCAGCAGCAGGTTCAATTTTCCCTGAAACCCCTCGGTTCTCAG 360
Db 328 TGGGGAACAACATTTACAGCAGCAGGTTTAATTTTCCCTGAAACCCCTGCAATTCACG 387
Qy 361 CATGGGGACAAGTGGGTCTCAAGTTCAGAGCAGCCAGAGCTCAGCCTCTCCACGCA 417
Db 388 CATGGGGACAAGTGGGTCTCAGGGGACAGACTCAGAGCTCAGCCTATGGGAGCA 444

RESULT 81
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LOCUS BQ61839 NIBB Mochii normalized Xenopus tailbud library Xenopus
DEFINITION laevis cDNA clone XL074d11 5', mRNA sequence.
ACCESSION BQ61839.1 GI:17423904
VERSION BQ61839
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 720)
REFERENCE Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
AUTHORS Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tehinigenes.nig.ac.jp.
Location/Qualifiers
1..720
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL074d11"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
/tissue_type="whole embryo"
/notes="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Mellicome/CRC Institute)."

BASE COUNT 230 a 135 c 158 g 197 t
ORIGIN
Query Match 16.9%; Score 342.8; DB 13; Length 720;
Best Local Similarity 71.9%; Pred. No. 3.6e-63;
Matches 476; Conservative 0; Mismatches 182; Indels 4; Gaps 2;

Qy 568 TCTGCCCCAGCGTCGAATCCACCCCGTCTTTGAAACAACTGAAGGCTGTCTACATCATCAGCTAC 627
Db 14 TTTGCCCTTCGTTGTTGAAGTGCAACCCAGTACTGGAGAACTGMAAGGCCATTAACAACTAC 73
Qy 628 AACCCGAAGAGTTTGAAGTGAATCTGAAAGCGGGGCTGTTCATCATCAGAGCTAC 687
Db 74 AATCCCAAGACTTTTGACTGGAGTCTAAAAAATGACAGAGTGTATTATATCAGAGCTAC 133
Qy 688 TCTGAGCAGCAGATCCACCGCTCCATTAAGTACTTCCATCTGGGTAGCAGACAGCAGGC 747
Db 134 TCTGAAGACGATATTTCATCGTTCTATAAGTACTCAATCTGGGTAGCAGCAGCAATGGC 193
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QY 748 AACAGGCGCTGGACAGCGCTTCCGCTGATGAGCGAGCGGCGCTCTACCTGCTC 807  
 Db 194 AATAAAGCTTTGGCTGCTTACCGATCTTTGAATGAAAGGCCACCTTTATTTACT 253  
 QY 808 TTCAGCGTCAATCGGAGTGGGCAATTTTGGGGTGGCCGAGATGAAGTCCCGCTGGAC 867  
 Db 254 TTCAGTGTAAATGGAAGTGGACATTTTGGGTGAGCTGAAATGAAGTCTGTTGGGAC 313  
 QY 868 TAGCGCACCAAGTCCCGGGTCTCGTCTCAGGCAAGTGGAGGGGAAGTTTGTATGCCAG 927  
 Db 314 TATAATGCTTATGCTGGAGTCTGGTCCAGGACAAATGGAAGGGAAGTTTGTATGAAA 373  
 QY 928 TGGATTTTGTAAAGATGATACCAATACACAGCTCCGCGACATCAGCTGGGAGATAAC 987  
 Db 374 TGGGCGCTTTGTCAAAGACGTACCTTAATACAGCTTGGCGATATTCGTTTAGAAAAATAC 433  
 QY 988 GACACAAACCGGTCAAAATCCCGGGACACCCAGGAGTGGCCCTTAGAAAAAGCCAAAG 1047  
 Db 434 GATAACAGCGCTGTACCACTCAAGGGACACTCAAGAGGTTCCCTTAGAAAAAGGCCAAG 493  
 QY 1048 CAAGTGTGAAATTTATCAGTTCTTACAAGCACACACCTCCATCTTTCGACGACTTTTGTCT 1107  
 Db 494 CRAAGTCTTAAATATGCAATGCTTCAAGCATACACCTCTATCTTTGATGACTTTGCA 553  
 QY 1108 CACTACAGAAAGCG-CCAGAGGAGGAGAGGTGGTGGCAAGGAACGGCAGAGTCGAAC 1166  
 Db 554 CATTATGAGAAGCGTCAAGAGGAGGAGGAGCCATGCGTAGGGA--GCAGAAATCGAAAC 610  
 QY 1167 AACAATGAGGGCGAACAGTTTCTTACATGTTCTTAACGTTTGACTTTGAAACAGTTTA 1226  
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 QY 1227 AA 1228  
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RESULT 82  
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 DEFINITION  
 laevis cDNA clone XL080n24 5', mRNA sequence.

ACCESSION  
 BJ064834  
 VERSION  
 BJ064834.1 GI:17480195  
 KEYWORDS  
 EST.  
 SOURCE  
 African clawed frog.

ORGANISM  
 Xenopus laevis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 Xenopodinae; Xenopus.

REFERENCE  
 1 (bases 1 to 706)  
 Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara  
 Y.

TITLE  
 Expressed genes in X. laevis embryo  
 JOURNAL  
 Unpublished (2001)  
 COMMENT  
 Contact: Tadasu Shin-i  
 Center For Genetic Resource Information  
 National Institute of Genetics  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshini@genes.nig.ac.jp.

FEATURES  
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 /note="vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs  
 were oligo-dT primed and directionally cloned. Staging

according to Nieuwkoop and Faber. Library is subtracted  
 and was constructed by N. Garrett and A.M. Zorn,  
 (Wellcome/CRC Institute). "

BASE COUNT 224 a 130 c 157 g 195 t

ORIGIN

Query Match 16.9%; Score 342.2; DB 13; Length 706;  
 Best Local Similarity 71.8%; Pred. No. 4.8e-63;  
 Matches 476; Conservative 0; Mismatches 183; Indels 4; Gaps 2;

QY 567 TTCTGCCCCCAGCGTCCGAATCCACCCCGTCTTGAATAAATGAAAGCGCTCACAAGCTA 626  
 Db 38 TTGCGCTTCTGGTTTGAAGTACACCCAGTACTGGAGAAATGGAAGCCCATTAACAAC 97  
 QY 627 CRAACCGAAGAGTTTGGAGTGGAAATCTGAAAAGCGGCGTGTTCATCATCAAGAGCTA 686  
 Db 98 TATCCCAAAGACTTTGAGTGGAGTCTAAAAAATGACGCTGTTTATCATCAAGAGCTA 157  
 QY 687 CTCTGAGGAGCATCCAGCGCTCCATTAAGTACTTCCATCTGTTAGCACAGACACGG 746  
 Db 158 CTCTGAGGAGCATTAATTCACCGTTCTATGAAGTACTCAATCTGGTGCAGTACTGAGCATGG 217  
 QY 747 CAACAAGCGCTGACAGCGCTTCCGCTGCATGACGACGCAAGGGCGCGCTCTACCTGCT 806  
 Db 218 CAATAAACGTTTGGATGCTGCTTACCGATCCTTGAATGAAAGGCCACTTTATTACT 277  
 QY 807 CTTACGCGTCAATGGAGTGGGCAATTTTGTGGGTGGCGGAGATGAAGTCCCGCTGGA 866  
 Db 278 CTTACGTTAAATGGAAGTGGACATTTTGTGGTGTAGCTGAAATGAAGTCTGTTGGA 337  
 QY 867 CTACGCGACAGTGGCGGGTCTGGTCTCAGGACAAGTGAAGGGGAAGTTTGTATGCCA 926  
 Db 338 CTATAATGCTTATGCTGGAGTCTGGTCCAGGACAAATGGAAGGAAAGTTTGTATGTC 397  
 QY 927 GTGGATTTTGTAAAGTGTACCCCAATACAGCTCCGCGACATCAGGCTGAGAGATAA 986  
 Db 398 ATGGGCTTTTGTCAAAAGACGTTCTTAATACCCAGTTGGCGCATATTCGTTAGAAATAA 457  
 QY 987 CGACAAACACCGGTCCACAACTCCCGGACACCCAGGAGTCCCTTAGAAAAAGCCAA 1046  
 Db 458 CGATAACAGCTTGTACCACTCAAGGGACACTCAAGAGGTACCCCTAGAAAGGCCAA 517  
 QY 1047 GCAAGTGTGAAATTTATCAGTTCTTCAAGCACACAACTCCATCTTTCGACACTTTGC 1106  
 Db 518 GCAAGTCTTAAATAATTTGCTATGTTCAGCATACAACTCTATCTTTGATGACTTTGC 577  
 QY 1107 TCCTACGAGAGCG-CCAGAGGAGGAGGTGGTGGCAAGGAGCGGAGTCCGAAA 1165  
 Db 578 ACATTATGAGAGCGTCAAGAGGAGGAGGAGCCATGCGTAGGGA---GAGAAATAGAAA 634  
 QY 1166 CAAACAATGAGGCGCAACCAAGTTTCTTACATGTTCTTAACCGTTTTCGACTTTGAAAACAGTTT 1225  
 Db 635 CAAACAATATCTGAGCGATATCTGCTATATATCACAACACTAATGATGACTCTGG 694  
 QY 1226 AAA 1228  
 Db 695 AAA 697

RESULT 83  
 BQ223830  
 LOCUS  
 DEFINITION  
 AGENCOURT\_7509852 NIH\_MGC\_92 Homo sapiens cDNA clone IMAGE:6042656  
 5', mRNA sequence.

ACCESSION  
 BQ223830  
 VERSION  
 BQ223830.1 GI:20405230  
 KEYWORDS  
 EST.  
 SOURCE  
 human.

ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
 1 (bases 1 to 883)  
 AUTHORS  
 NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM13282 row: 9 column: 09 High quality sequence stop: 684.

## FEATURES

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/lab_host="DH10B (phage-resistant)"
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Site 2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 2.5 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."
285 a 176 c 200 g 218 t 4 others
BASE COUNT
ORIGIN

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Query Match	16.8%	Score 340.6;	DB 14;	Length 883;
Best Local Similarity	74.6%	Pred. No. le-62;		
Matches 441;	Conservative	0;	Mismatches 149;	Indels 11;
Gaps 1;				

	QY	583	GAATCCACCCTTCCTTGGAAAACATGTAAGGTGCTCACNGCTACAAACCGGAAGAAGTTT	642
	DB	35	GAAACCCCACCCAGTGTTGGGAGAAGCTTCGGTGCCATTATAAACAATTATAACCCCCAAAGAATTTT	94
	QY	643	GAGTGGAACTCTGA AAAACGCGGGCTGTGTTTCATCATCAAGAGCTACTCTCAGGACGACATC	702
	DB	95	GACTGGNATCTGA AANATGCGCGGTTTTTCATCATTAAGAGCTACTCTCAGGACGATAAT	154
	QY	703	CACCGCTCCATTAA GTACTCCATCTCGTGTPAGCACAGACACGGCAAACAGCGCTCGGCAC	762
	DB	155	CACGTTCCATTAA GTATAATAATTTGGTGACACAGAGCATGGTAAACAAGAGACTGGAT	214
	QY	763	AGCGCTTCGGCTG ATGACGACGAGAAGGGGCCGTCTACTCGTCTTTACAGCTCAATGGG	822
	DB	215	GCTGCTTATCGTT CCAATGAACGGGAAGGCCCGTTTACTTACTTTTCAGTGTCAACGCG	274
	QY	823	AGTGGGCAATTTTG TCGGGTGGCGGAGATGAAGTCCCGCTGGACATACGGCAACCACTGCC	882
	DB	275	AGTGGACATTTCT GTGCGTGGCAGAAATGNAATCTGCTGTGGACTACAAACACATGTGCA	334
	QY	883	GGGGTCTGGTCTC AGGACAAAGTGGAAAGGGGAAGTTTTGATGTCGCAGTGGATTTTTGT	942
	DB	335	GGTGTGTGGTCCC AGGACAAATGGAAGGGTCGTTTTGATGTCAGGTGGATTTTTGTGAAG	394
	QY	943	GATGTATCCCAAT AACACAGCTTCGGGCACATCAGAGCTGGAGAAATACGACAAACCGGTC	1007
	DB	395	GAGCTTCCCAATA TAGCCNACTGCGCACATTCGCGCTAGAGAACCAACGAGAATAAACCCG	454
	QY	1003	ACAAACTCCCGGCA CCCCAGGAGTGCCTTAGAAAAAGCCCAAGCAAGTGTGGAATTT	1067
	DB	455	ACCACTCTAAGGGA CATCAGGAAGTGCCTCTGGAAAGGCTAAGCAGGTGTGGAATAAT	514
	QY	1063	ATCAGTTTCTTACA AGCACACAACTCCATCTTCGACGACTTTGCTCACTACGAGAACGCG	1127
	DB	515	ATAGCCAGCTACA AGCACACCACTTCCATTTTGTGACTTCTTCACACTATAGAAAAACG	574
	QY	1123	C-AdAGAGGAGGAG TGTTGGTCCGCAAGGAACGGCAGAGTCGAAACAAACAA	1172
	DB	575	CAAGAGGAAGCA GAAGTAGTTTAAAAAGGAACGTCGAAGTCTGGGGAAAAATA	625

RESULT 84  
BH353078/c  
LOCUS

DEFINITION CH230-163C17.TV CHORI-230 Segment 1 *Rattus norvegicus* genomic clone CH230-163C17, DNA sequence.

ACCESSION BH353078

VERSION BH353078.1

KEYWORDS GI:17283812 GSS.

REFERENCES	SOURCE	ORGANISM
1. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 111-120 (1981).	1	<i>Staphylococcus aureus</i>
2. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 121-128 (1981).	2	<i>Staphylococcus aureus</i>
3. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 129-136 (1981).	3	<i>Staphylococcus aureus</i>
4. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 137-144 (1981).	4	<i>Staphylococcus aureus</i>
5. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 145-152 (1981).	5	<i>Staphylococcus aureus</i>
6. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 153-160 (1981).	6	<i>Staphylococcus aureus</i>
7. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 161-168 (1981).	7	<i>Staphylococcus aureus</i>
8. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 169-176 (1981).	8	<i>Staphylococcus aureus</i>
9. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 177-184 (1981).	9	<i>Staphylococcus aureus</i>
10. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 185-192 (1981).	10	<i>Staphylococcus aureus</i>
11. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 193-200 (1981).	11	<i>Staphylococcus aureus</i>
12. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 201-208 (1981).	12	<i>Staphylococcus aureus</i>
13. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 209-216 (1981).	13	<i>Staphylococcus aureus</i>
14. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 217-224 (1981).	14	<i>Staphylococcus aureus</i>
15. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 225-232 (1981).	15	<i>Staphylococcus aureus</i>
16. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 233-240 (1981).	16	<i>Staphylococcus aureus</i>
17. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 241-248 (1981).	17	<i>Staphylococcus aureus</i>
18. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 249-256 (1981).	18	<i>Staphylococcus aureus</i>
19. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 257-264 (1981).	19	<i>Staphylococcus aureus</i>
20. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 265-272 (1981).	20	<i>Staphylococcus aureus</i>
21. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 273-280 (1981).	21	<i>Staphylococcus aureus</i>
22. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 281-288 (1981).	22	<i>Staphylococcus aureus</i>
23. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 289-296 (1981).	23	<i>Staphylococcus aureus</i>
24. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 297-304 (1981).	24	<i>Staphylococcus aureus</i>
25. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 305-312 (1981).	25	<i>Staphylococcus aureus</i>
26. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 313-320 (1981).	26	<i>Staphylococcus aureus</i>
27. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 321-328 (1981).	27	<i>Staphylococcus aureus</i>
28. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 329-336 (1981).	28	<i>Staphylococcus aureus</i>
29. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 337-344 (1981).	29	<i>Staphylococcus aureus</i>
30. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 345-352 (1981).	30	<i>Staphylococcus aureus</i>
31. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 353-360 (1981).	31	<i>Staphylococcus aureus</i>
32. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 361-368 (1981).	32	<i>Staphylococcus aureus</i>
33. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 369-376 (1981).	33	<i>Staphylococcus aureus</i>
34. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 377-384 (1981).	34	<i>Staphylococcus aureus</i>
35. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 385-392 (1981).	35	<i>Staphylococcus aureus</i>
36. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 393-400 (1981).	36	<i>Staphylococcus aureus</i>
37. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 401-408 (1981).	37	<i>Staphylococcus aureus</i>
38. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 409-416 (1981).	38	<i>Staphylococcus aureus</i>
39. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 417-424 (1981).	39	<i>Staphylococcus aureus</i>
40. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 425-432 (1981).	40	<i>Staphylococcus aureus</i>
41. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 433-440 (1981).	41	<i>Staphylococcus aureus</i>
42. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 441-448 (1981).	42	<i>Staphylococcus aureus</i>
43. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 449-456 (1981).	43	<i>Staphylococcus aureus</i>
44. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 457-464 (1981).	44	<i>Staphylococcus aureus</i>
45. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 465-472 (1981).	45	<i>Staphylococcus aureus</i>
46. J. H. J. van den Bosch, <i>et al.</i> , <i>Antonie van Leeuwenhoek</i> 47: 473-480 (1981).	46	<i>Staphylococcus aureus</i>
47. J. H. J. van den Bosch,		

Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa;  
Mammalia; Eutheria;  
Rodentia; Sciurognathi;  
Muridae; Murinae;  
Rattus;  
Rattus.

## REFERENCE AUTHORS

A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P., and Fraser, C.M.

**TITLE**  
**JOURNAL**

UNPUBLISHED (1999)  
Other GSSs: CH230-163C17.TJ  
Contact: Shaving Zhao

The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208

Fax: 302 336 0200  
 Email: szhao@tigr.org  
 Clones are derived from the rat BAC library CHO81-210

clones are derived from the rat BAC library CHORI-230 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library availability please contact Dieter de Jong ([dieter@chori.org](mailto:dieter@chori.org)).

Clones may be purchased from BACPAC Resources  
 Availability, please contact Fletcher de Jong (pdejong@mail.cno.org),  
 (<http://www.chori.org/bacpac/> for aising information from BAC and

page: [http://www.tigr.org/tdb/bac\\_ends/rat/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html)  
<http://www.ncbi.nlm.nih.gov/Trac/seq/blast.cgi>

Plate: 163 row: 1  
Seq primer: T7

## FEATURES

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1. .739
/organism="Rattus norvegicus"
/strain="BN/SnHsd/MCw"
/db_xref="taxon:10116"
/clone="CH230-163C17"
/clone_lib="CHORI-230 Segment"
/sex="Female"
/cell_type="Brain"
/note="Vector: pTARBAC2.1; Si
CHORI-230 Rat (BN/SnHsd/MCw)
Pieter de Jong"

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Matches 493;	Conservative 0;	Mismatches 200;	Indels 4;	Gaps 2;
Qy	469	CAGACCCGCTGGGTGCCCCACGCAACAGAAACGCGCGCTTTCGGCGAGAGCGGAGGGGCT	528	
Db	708	CAGATCGTTGGGTAGTCTCTCGGATAGGGGAACCGGCTTCAACAGAACATGGGAACA	649	
Qy	529	GGCAGCGATAGCAACTCTCTCGTGAAGCGTCAAGCGTAAATTCTGCCC---	585	
Db	648	GGCAGTGAAGAACTTTGGTTTGGTGTGTGTACCTGTTAGTGTCTTCACTCTCTAGTGTAGAG	589	
Qy	586	TCCACCCCGCTCTTTGAAAAAATGAAAGCGTGTCCACAGCTACAAACCCGAAAGAGTTTGGAG	645	
Db	588	GTGCATCCAGTGTGGAAAAAATTAAGGCCATAAAACAATTATTAATCCCAAGACTTTTGAT	529	
Qy	646	TGGAATCTGAAAACGGGGCGTGTGTTTCATCATCAAGAGCTACTCTGTAGAGACGACATCCAC	705	
Db	528	TGGAACCTGGAAGATGAGACGTGTGTTTATTAATTAAGAGCTATTCTGTAGGATGATATACAC	469	
Qy	706	CGCTCCATTAAAGTACTCCATCTGGTGTGACACAGAGACACGGCAACAAAGCGCTCGGACAGC	765	



/lab\_host="DH108"  
/note="vector: p773D-Pac (Pharmacia) with a modified  
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was prepared from mRNA obtained from pooled 8-9 week  
(total) fetus material with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAGTGGAGGCGGCTTAATTTTCTTTTCTTTT 3']  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p773 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 85 a 104 c 97 g 69 t  
ORIGIN

Query Match 16.6%; Score 336.8; DB 9; Length 355;  
Best Local Similarity 99.1%; Pred. No. 7.4e-62;  
Matches 349; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
Qy 519 CGGAGGGGCTGGCAGCGATAGCAACTCTCTGGAACTCCAGGCTAATTTCTGCCCCAG 578  
Db 5 CGGAGGGGCTGGCAGCGATA-CAACTCTCTGGAACTCCAGGCTAATTTCTGCCCCAG 63  
Qy 579 CGTGGATCCACCCCGCTTGAATACTGAAGCTGCTCACAGCTACACCCGAAAGA 638  
Db 64 CGTGGATCCACCCCGCTTGAATACTGAAGCTGCTCACAGCTACACCCGAAAGA 123  
Qy 639 GTTTGAGTGGAAATCTGAAAGCGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGA 698  
Db 124 GTTTGAGTGGAAATCTGAAAGCGGCGTGTGTTTCATCATCAAGAGCTACTCTGAGGACGA 183  
Qy 699 CATCCACCGCTCCATTAAGTACTCATCTGTTGATGACACAGACGCGGCGCT 758  
Db 184 CATCCACCGCTCCATTAAGTACTCATCTGTTGATGACACAGACGCGGCGCT 243  
Qy 759 GGACAGCGCTTCCGCTGCATGACAGACAGGCGGCGCTTACCTGCTCTTCAGCGTCAA 818  
Db 244 GGACAGCGCTTCCGCTGCATGACAGACAGGCGGCGCTTACCTGCTCTTCAGCGTCAA 303  
Qy 819 TGGGAGTGGGCAATTTTGTGGGGTGGCCGAGATGAAGTCCCGCTGGGACTAC 870  
Db 304 TGGGAGTGGGCAATTTTGTGGGGTGGCCGAGATGAAGTCCCGCTGGGACTAC 355

RESULT 87  
BQ899696  
LOCUS  
DEFINITION  
5', mRNA sequence.  
ACCESSION  
BQ899696  
VERSION  
BQ899696.1 GI:22291698  
KEYWORDS  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 937)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-x@mail.nih.gov  
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,  
Ph.D.  
cDNA Library Preparation: ResGen, Invitrogen Corp  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM13885 row: f column: 18  
High quality sequence stop: 741.  
Location/Qualifiers  
1. .937

/organism="Mus musculus"  
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/clone="IMAGE:6393617"  
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/notes="Organ: oocytes; Vector: pCMV-SPORT6.1.ccd; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.95 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH MGC library."  
BASE COUNT 261 a 222 c 242 g 205 t 7 others  
ORIGIN  
Query Match 16.6%; Score 336.2; DB 14; Length 937;  
Best Local Similarity 74.7%; Pred. No. 9.1e-62;  
Matches 422; Conservative 0; Mismatches 143; Indels 0; Gaps 0;  
Qy 583 GAATCCACCCCGCTTGGAAAACTGAAAGCTCTCACAGCTACAAACCCGAAAGTTT 642  
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Qy 643 GAGTGGAAATCTGAAAGCGGCGTGTTCATCATCAAGAGCTACTCTGAGGACGATC 702  
Db 352 GACTGGAAATCTGAAACATGCGCGGTTTTTCATCATTAAGAGCTACTCTGAGGACGATC 411  
Qy 703 CACCGCTCCATTAAGTACTCCATCTGGTGTAGCACAGACGCGCAACAGCGCTTGAC 762  
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Qy 763 AGCCCTTCGCTGCATGAGACGAGGCGCGTCTACCTGCTCTTCAGCGTCAATGGG 822  
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Qy 823 AGTGGGCAATTTTGTGGGGTGGCGGATGAAGTCCCGCTGGAGTACGCGACGAGTGC 882  
Db 532 AGTGGACATTTCTGTGGAGTTGCAGATGAATCTCTGTGGACTACACACATGTGCA 591  
Qy 883 GGGGTCTGGTCTCAGGACAAAGTGGAGGGGAAAGTTTTCATGTCTCCAGTGGATTTTGTAAAG 942  
Db 592 GGTGTGGTCCAGGACAAATGGAAGGTCGTTTCGATGTGATGATGATTTTGTGAAG 651  
Qy 943 GATGTACCAATTAACAGCTCCGCGACATCAGGCTGGAGAAATACGACAAACCCGGTC 1002  
Db 652 GACGTTCCCAATAGCCAACTCGCACACATTCGCTAGAGAAACACGAGAAATAAACCATG 711  
Qy 1003 ACAAACTCCCGGACACCCAGGAGTCCCTTAGAAAAAGCAAGCAAGTCTGCAAAATT 1062  
Db 712 ACCAACTCTAGGACATCTAGGAAAGTCCCTCTGAAAAAGCTAAGCAGGTGTTGAAATC 771  
Qy 1063 ATCAGTTCTTCAAGCACACAACTCCATCTTCGACGACTTTGCTCACTACGAGAACGC 1122  
Db 772 ATAGCCAGCTACAAGCACACCACTTCCATTTTGTGATGACTTTCACACTATGAGAAACGC 831  
Qy 1123 CAGAGGAGGAGGAGTGGTGGCGAA 1147  
Db 832 CAAGAGGGAAGAAGAGTGTAA 856  
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BQ063156  
LOCUS  
DEFINITION  
719 bp mRNA linear EST 07-DEC-2001  
BQ063156 NIBB Mochii normalized Xenopus tailbud library Xenopus  
laevis cDNA clone XL070e20 5', mRNA sequence.  
ACCESSION  
BQ063156  
VERSION  
BQ063156.1 GI:17422181  
KEYWORDS  
EST.  
SOURCE  
African clawed frog.  
ORGANISM  
Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
Xenopodinae; Xenopus.  
1 (bases 1 to 719)  
REFERENCE  
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara

```
.
TITLE
JOURNAL
COMMENT

Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .719
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL070e20"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/notes="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute). "
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BASE COUNT      230 a   135 c   157 g   196 t       1 others
ORIGIN

Query Match      16.6%; Score 336; DB 13; Length 719;
Best Local Similarity 71.2%; Pred. No. 1e-61;
Matches 472; Conservative 0; Mismatches 186; Indels 5; Gaps 2;

QY 568 TCTGCCCCAGCGTCGAATCCACCCCGTCCTTGA AAAACTGAAGGCTGCTCACAGCTAC 627
DB 14 TTTGCCTTCCTGTTGAAGTGCAACCCAGTACTGGAGAACTGAAGCCATTAACTAC 73

QY 628 AACCCGAAGAGTTTGAGTGGAACTCTGA AAAGCGGCGTGTTCATCATCAGAGCTAC 687
DB 74 AATCCCAAGACTTTGACTGGAGTCTAAAAAATGGACAGTGTATTATCAAGAGCTAC 133

QY 688 TCTGAGGACGACATCCACCGCTCCATTAACTACTCCATCTGGTGTAGCAGAGCAGCGG 747
DB 134 TCTGAAGACCATATTCATCGTTCTATAAGTACTCAATCTGGTGTAGCAGCCGACATGGC 193

QY 748 AACAGCGCTGGACAGCGCTTCGCTGTCATGAGCAGCAAGGGCGGCTACCTGCTC 807
DB 194 AATAAGCTTTGATGCTGCTTACCGATCTTTGAATGGAAGGCCACCTTTATTACTC 253

QY 808 TTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCCGAGATGAAGTCCCCCGTGGAC 867
DB 254 TTCAGTGTAAATGGAAGTGGACATTTTGTGGTGTAGCTGAAATGAAGTCTGTTGGAC 313

QY 868 TAGCGCACAGTCCGGGTCTGGTCTCAGGACAAGTGGAGGGAAGTTTGATGCCAG 927
DB 314 TATAATGCTTATGCTGGAGTCTGGTCTCCAGACAATGGAGGGAAGTTTGATGTA AAA 373

QY 928 TGGATTTTGTAAAGATGTACCAATAAACAGCTCCGGCACATCAGCGTGGGAGATAAC 987
DB 374 TGGGCTTTGCTCAAGACGTAACCTAATAACAGTTGGCGCATATTCGTTAGAAATAAC 433

QY 988 GACAACAAACGGGTACAACCTCCGGGACACCCAGAGGTGCGCTTTAGAAAAAGCCAAG 1047
DB 434 GATAACAAGCCTGTACCAACTCAAGGACACACTCAAGAGGTTCCTCCTAGAAAAAGGCCAAG 493

QY 1048 CAAGTCTGAATATTACGTTCTTACAGCAGACACACCTCCATCTTCGACGACTTGGCT 1107
DB 494 CAAGTCTTAAAAATAATTTGCAATGTTCAAGCATACAACCTCTATCTTTGATGACTTTGCA 553

QY 1108 CACTACAGAAA--GCGCCAGAGGAGGAGGTGGTGCAGGAAGCAAGCGCAGAGTCCAAA 1165
DB 554 CATTATGAGNAGGCTCAAGAGGAGGAGGAGCCATCGGTAGGGA---GCGAATCGAAA 610

QY 1166 CAACAATAGGGCGCAACCAAGTTTCTTTACATGTTTCTAACGTTTGACTTTTGAAACAGTTT 1225
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Db 611 CAACAATATCTCGAGCGATATCTCTGCTATATATCACACACTAATGATGTAGACTCTGG 670
QY 1226 AAA 1228
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Db 671 AAA 673

RESULT 89
BE026361
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DEFINITION
db37f12.y1 Blackshear/Soares normalized Xenopus egg library Xenopus
laevis cDNA clone IMAGE:3300719 5', similar to TR:064536 O64536
YU8H12R.13 PROTEIN. ; mRNA sequence.
BE026361
VERSION BE026361.1 GI:8319722
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 632)
REFERENCE
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
WashU Xenopus EST project, 1999
Unpublished (1999)
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Bento Soares and M. Fatima Bonaldo
(University of Iowa). DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 456.
Location/Qualifiers
1. .632
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/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
/notes="Vector: pTTT3-Pac; Site_1: EcoRI; Site_2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
pTTT3-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subtraction: two
approaches to facilitate gene discovery', Genome Research
6:791-806, 1996. The first strand synthesis used a
NotI-drr18 primer; double stranded cDNAs were ligated to
EcoRI adapters, digested with NotI, and directionally
cloned into the NotI and EcoRI-digested pTTT3-Pac vector.
The library contained approximately 7.2 X 105
recombinants, with average insert sizes of 1-1.5 kb."
BASE COUNT      160 a   188 c   162 g   121 t       1 others
ORIGIN

Query Match      16.5%; Score 335.6; DB 10; Length 632;
Best Local Similarity 75.4%; Pred. No. 1.3e-61;
Matches 432; Conservative 0; Mismatches 135; Indels 6; Gaps 1;
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Qy 406 CCTCTCCAGCAGACGCCGCCAGCTTTGGCTCAACGGCAGTATCAGAGCCCTCAGCAGCCA 465
Db 66 CCGCGCTGTCTCAGACTCAATACCAAATCCACGGCCCTCAACAGCAGCCACAGGCC 125
Qy 466 CCCAGACCCGCTGGTTGGCCCGCAGCAACAGAAACGGCGGTTTGGGCGAGCGGAGGG 525
Db 126 CCTCAGATCCTGGTGGCCCGCAGGAGTAAAGAACGCTGCTTATGGTCAGGGTGGAGGC 185
Qy 526 GCTGGCAGCAGATAGCAACTCTCTCGGAAACGTCAGAGCCATAATCTGCCCCCGCAGGTCGAA 585
Db 186 CCA-----GATGGGAACCTCTGGGAGGAGCCAGTCTCAGCTGCCCCCGGAAATGAG 239
Qy 586 TCCACCCCGCTCTTGAAMAACTGAAGCTGCTCAGCTCAGCTACACCCGAAAGAGTTTGAG 645
Db 240 TCTCACCTGTGCTAGAGAAACTGAAGGCGCCCAACAGCTACAAACCCCAAGGACTTTGAC 299
Qy 646 TGGAACTGAAAGCGGCGGTGTTTCATCATCAAGAGCTACTCTGAGGAGCAGATCCAC 705
Db 300 TGGAACTGAAAGCGGCGGTGTTTATAATAAAGAGCTACTCTGAGGATGATATCCAC 359
Qy 706 CGCTCCATTAAGTACTCCATCTGTGTGTAGCAGACGCGCAACAGCGCTCGACAGC 765
Db 360 GGTTCATCAATACTCCATCTGTGTGACGACAGCAGCATGGGAATAAAGCTTGGATAAC 419
Qy 766 GCCTTCGCTCAGCAGCAGCAAGGGGCGCTCTACTCTCTCAGGTCATNTGGAGT 825
Db 420 GCTTTCCGCTCCATGAATGGAAGGCGCCGCTACTACCTTCTGTTCAGCGTCAACGGCAGT 479
Qy 826 GGGCATTTTCTGGGGTGGCGAGTGAAGTCCCGGTGAGTACGACAGCAGGCGCGGG 885
Db 480 GGACACTTTTCCGGGCTAGCCGAGTGAAGTCCCGGTGAGTATGGCAGCAGTGGCCGT 539
Qy 886 GTCTGGTCTCAGGACAACTGGAAGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGAT 945
Db 540 GTCTGGTCAAGGACAACTGAAGGCGCAAGTNGCTCAAGTGGCTTTGTCAAGGAC 599
Qy 946 GTACCCCAATACAGCTCCGCGACATCAGGCTG 978
Db 600 GTTGCCAAACAGCTGAGGACATCGCCTG 632

RESULT 90
BQ232423
LOCUS
DEFINITION BQ232423 873 bp mRNA linear EST 02-MAY-2002
5', mRNA sequence.
AGENCY: NIH-MGC
ACCESSION BQ232423
VERSION BQ232423.1
KEYWORDS BQ232423.1 GI:20413823
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 873)
NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@rs-research.nih.gov
Tissue Procurement: ATCC/DCTP/DRP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13314 row: b column: 15
High quality sequence stop: 715.

FEATURES
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/clone="IMAGE:6054830"
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT 251 a 207 c 220 g 195 t
ORIGIN
Query Match 16.5%; Score 335.2; DB 14; Length 873;
Best Local Similarity 67.8%; Pred. No. 1.5e-61;
Matches 488; Conservative 0; Mismatches 228; Indels 6; Gaps 1;
Qy 416 CACAGCCCCAGCTTTGGCTCAACCGCAGTATCAGAGCCCTCAGCAGCCACCCAGACCC 475
Db 105 CTCACCTCCACACAGCCTGCCAGCTTTTCAGTCCAGCAACAGGAGCTCAGCCAAACC 164
Qy 476 GCTGGTGGCCCAACGCAACAGAAACCGCGGTTTGGGCGAGCGGAGGCGCTGGCAGCG 535
Db 165 GCTGGGTAGCACCTCGGAACCGGTGGCAGTGGGTTCCGTCATATGGGGTGGATGTAATG 224
Qy 536 ATACCAACTCTCTCGGAAACGTCACAGCCTAAATCTGCCCCCAGCGTCGAATCCCAACCCCG 595
Db 225 GAGTAGACAGCTCTCAGCGTGGTTCTGGATCTACTCTTC-----AGAACCCCAACCCAG 278
Qy 596 TCCTTGAAGAACTGAAGGCTGCTCACAGCTACAAACCCGAAAGAGTTTGAAGTGAATCTGA 655
Db 279 TGTGGAGAGCTTCGCTCCATTAATAACTATAACCCCAAGATTTTGAAGTGAATCTGA 338
Qy 656 AAACGGGGGTGGTTTCATCATCAAGAGCTACTCTGAGGAGCAGCATCCACGGCTCCATTA 715
Db 339 AACATGCGCGGTTTTCATCATTAAGAGCTACTCTGAGGAGCAGATATTCACCGTTTCCATTA 398
Qy 716 AGTACTCCATCTGTGTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 775
Db 399 AGTATAATATTTGGTGACGACAGAGCATGGTAAAGAGAGCTGGATGCTGCTTATCGTT 458
Qy 776 GCATGAGCAGCAGGCGCGCTCTACCTGCTCTTACCGCTCAATGGGAGTGGGCAATTTT 835
Db 459 CCATGAACGGGAAGGCCCGCTTTTACTTTTCACTGTCACGCGCAGTGGACACTTCT 518
Qy 836 GTGGGTGGCGGAGATGAAGTCCCGCTGAGCTACGGCAGCAGTCCCGGGGTCTGGTCTC 895
Db 519 GTGGCGTGGCAGAAATGAAATCTCTGTGGACTACAACACATGTGCGAGGTGTGTGGTCCC 578
Qy 896 AGGACAAAGTGAAGGGAAGTTTGATGTCCAGTGGATTTTGTAAAGGATGTACCCCAATA 955
Db 579 AGGACAAATGAAGGGTCGTTTTGATGTCAAGTGGATTTTGTGAGAGACGTTCCCAATA 638
Qy 956 ACCAGCTCCGGCAGCATCAGGCTGGAGAAATACGACAAACCGGTCACAAACTCCCGGG 1015
Db 639 GCCAACTGGCAGACATTCGCTAGAGAAACAGAGATAAACAGTGCACCACTCTAGGG 698
Qy 1016 ACACCGAGGAGTCCCTTAGAAAAGCCAGAGCAGTGTGAAAATTTATCAGTTCCTACA 1075
Db 699 ACACAGGAAGTCCCTCTCGAAAAGGCTAAGCAGGTTTGAATAATTTATAGCCAGCTACA 758
Qy 1076 AGCACAAACCTCCATCTCTGAGCAGCTTTGCTCACTACGAGAGCGCCAGAGAGGAGGA 1135
Db 759 AGCACAACTTCCATTTTGTGATGACTTCTCACACTATGAGAAACGCCCAAGAGAGGAAGA 818
Qy 1136 GG 1137
Db 819 AG 820

RESULT 91
H69270
LOCUS
DEFINITION H69270 Homo sapiens cDNA clone HE6WCR115 5', mRNA sequence.
ACCESSION H69270
VERSION H69270.1
GI:1030687
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KEYWORDS EST. human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 363)  
AUTHORS Jay, P.  
TITLE Human cDNAs from HESW library  
JOURNAL Unpublished (1995)  
COMMENT Other ESTs: T90361  
Contact: Jay, P.  
Centre de Recherches de Biochimie Macromoléculaire  
Centre National de Recherches Scientifiques (CNRS)  
1919 route de Mende, 34033 Montpellier, France  
Tel: 3367613349  
Fax: 3367521559  
Email: pj@merlin.crbm.cnrs-mop.fr  
Seq primer: T3.  
FEATURES  
source  
1..363  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/map="20p11"  
/clone="HE6WCR115"  
/note="HE6WCR115"  
/note="Vector: lambda zap; Site 1: EcoRI; Site 2: XhoI; using an oligodT-XhoI primer. After second strand synthesis, an EcoRI adaptor was ligated and the cDNA was size selected on an agarose gel before directional cloning in the EcoRI and XhoI sites of lambda Zap vector."  
BASE COUNT 111 a 83 c 95 g 70 t 4 others  
ORIGIN  
Query Match 16.4%; Score 333.4; DB 14; Length 363;  
Best Local Similarity 98.1%; Pred. No. 48-61; Mismatches 2; Gaps 2;  
Matches 356; Conservative 0; Indels 5; Indels 2; Gaps 2;  
QY 873 CACCAGTGC CGGGGTCTGGTCTCAGGACAAAGTGGAAAGGGGAAGTTTGATGTC CAGTGGAT 932  
DB 1 CACCAGTGC CGGGGTCTGGTCTCAGGTCAGTCAAGTGGAAAGGGGAAGTTTGATGTC CAGTGGAT 60  
QY 933 TTTTGTAAAGGATGATCCCAATACCAGTCCCGGCACATCAGGCTCGAGAGTAACGACAA 992  
DB 61 TTTTGTAAAGGATGATCCCAATACCAGTCCCGGCACATCAGGCTCGAGAGTAACGACAA 120  
QY 993 CAACCGGTACAACTCCGGGACACCCAGAGGTGCCCTTAGAAAACCCCAAGCAAGT 1052  
DB 121 CAACCGGTACAACTCCGGGACACCCAGAGGTGCCCTTAGAAAACCCCAAGCAAGT 180  
QY 1053 GCTGAAAATTTATCAGTTCTCTACAGACACAACTCCATCTTCGACGACTTTGCTCACTA 1112  
DB 181 GCTGAAAATTTATCAGTTCTCTACAGACACAACTCCATCTTCGACGACTTTGCTCACTA 240  
QY 1113 CGAAGACGCGCA - GAGGAGGAGGAGTGTGCGCAAGGACCGCAGAGTCGAAACAAACA 1171  
DB 241 CGAAGACGCGCAGGAGGAGGAGTGTGCGCAAGGACCGCAGAGTCGAAACAAACA 300  
QY 1172 ATGAGGCGAACAGATTCTTACATGTTCTAAAGTTTGAATTT - GAACAGTTTAAAC 1230  
DB 301 ATGAGGCGAACAGATTCTTACATGTTCTAAAGTTTGAATTTGACATTTTGGAAACAGATTAAAC 360  
QY 1231 ACG 1233  
DB 361 ACG 363  
RESULT 92  
LOCUS BQ899797  
DEFINITION AGENCOURT\_8749084 NIH\_MGC\_130 Mus musculus cDNA clone IMAGE:6334535  
ACCESSION BQ899797  
VERSION BQ899797.1 GI:22291811

KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 943)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman, Ph.D.  
cDNA Library Preparation: ResGen, Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LLAM13795 row: h column: 24  
High quality sequence start: 21  
High quality sequence stop: 530.  
FEATURES  
source  
1..943  
Location/Qualifiers  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:6334535"  
/lab\_host="NIH MGC 130"  
/note="Organ: otocysts; Vector: pCMV-SPORT6.1.cdb; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.95 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH MGC Library."  
BASE COUNT 173 a 305 c 265 g 199 t 1 others  
ORIGIN  
Query Match 16.4%; Score 333.4; DB 14; Length 943;  
Best Local Similarity 86.6%; Pred. No. 3.6e-61; Mismatches 367; Conservative 0; Indels 0; Gaps 0;  
QY 1 CAAAGGACAAATATAAAGTACAAATGGTTCGTATCATCAGAGGATACAGTTTCATG 60  
DB 228 CAAAGGACAAATATAAAGTACAAATGGTTCGTATCATCAGAGGATACAGTTTCATG 287  
QY 61 ACAATGACTTTGAGCCCTACCTTACCTGAGCAGTCAATCAGAGTAAACAGTACCCCTCAA 120  
DB 288 ACAATGACTTTGAGCCCTACCTTACCTGAGCAGTCAATCAGAGTAAACAGTACCCCTCGA 347  
QY 121 TGAGCGACCCCTACCTGTCAGCTATTACCGCGCTCCATTGGATTTCCTTACTCCCTCA 180  
DB 348 TGAGTGATCTTACCTGTCAGTTCCTATCCACCATCCATTGGATTTCCTTACTCCCTCA 407  
QY 181 ATGAGGCTCGGTGTTACTGAGGGGACCTCCGATTCATACCTCACCACCTACGGAC 240  
DB 408 GCAGGACCATGTCCTCACTGCGGGGACCTCCCATCCGCTATCTCATTACCTATGGAC 467  
QY 241 AGCTCAGTAAACGAGACCATCATTTTATGACGATGCTGTTTTGGGACGCTCGGGGCC 300  
DB 468 AACTTAGTAAATGAGACCATCACTTCATGATGATGCTGTTTTGGGACGCTCGGGGTC 527  
QY 301 TGGGGAACAACATCTATCAGCACAGGTTCAATTTTTTCCCTGAAAAACCCCTGCGTTCTCAG 360  
DB 528 TGGGGAACAACCTTTTACCAGCACAGGTTTAAATTTTTTCCCTGAAAAACCCCTGCGATTCTCAG 587  
QY 361 CATGGGGGACAGTGGGTCTCAAGGTTCAGAGACCCAGAGCTCAGGCTCTCCAGACAG 420  
DB 588 CATGGGGGACCGTGGTTCTCAGGGGACGAGACTCAGAGCTCAGGCTATGGAGGAGTT 647  
QY 421 CCCC 424  
DB 648 ACCC 651

```

RESULT 93
AA636479
LOCUS
DEFINITION v18d03.r1 Barstead mouse myotubes MPLRB5 linear EST 22-OCT-1997
            542 bp mRNA Mus musculus cDNA clone
IMAGE:1120997.5, mRNA sequence.
ACCESSION
VERSION AA636479.1 GI:2560258
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 542)
Marra, M., Hallier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, F., Lennon, G., Soares, B., Wilson, R. and
Waterson, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:610333
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 512.
Location/Qualifiers
1..542
/organism="Mus musculus"
/strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:1120997"
/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
/notes="vector: p77T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCAGCAATCTGAAGTGGGAGCGCGCGCTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATTCGATCCITG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified p77T3 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."
BASE COUNT 131 a 152 c 134 g 125 t
ORIGIN
Query Match 16.4%; Score 333; DB 9; Length 542;
Best Local Similarity 89.0%; Pred. No. 4,7e-61;
Matches 371; Conservative 0; Mismatches 45; Indels 1; Gaps 1;
Qy 1 CAAAGGACAGATAATAAAGTACAAATGGTTCCTTACATCAGAGGATACAGTTTCATG 60
Db 116 CAAAGGACAGATAATAAAGTACAAATGGTTCCTTTCATCAGAGGATACAGTTTCATG 175
Qy 61 ACATGACTTTGAGCCCTACCTTACTGACAGATCAATCAGATGACAGTTACCCCTCAA 120
Db 176 ACAATGACTTTGAGCCCTACCTTCTTGACAGATCAATCAGATGACAGTTACCCCTCGA 235
Qy 121 TGAGGACCCCTACCTGTCACAGTATTATCCGCCCTGTCATGGATTCTCTTACTCCCTCA 180
Db 236 TGAGTGATCCTTACCTGTCAGTACTACTCCACCATCAATGGATTCTTACTCTCCCTCA 295
Qy 181 ATGAGGCTCGGTGTTACTATGCGAGGGGACCCCTCCGATTCCATACCTACCCACCTACGGAC 240

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Db 296 GCGAGGCACCATGTCCTCCACTCCAGGGA-CCTCCCATCCCTGATCTCTCACTACCTATGAC 354
Qy 241 AGCTCAGTAACGAGAGACCATCATTTTATGCAGATGCTGTTTTTTGGGAGAGCTCTGGGGGCC 300
Db 355 AACTAGTATGAGAGACCATCATCTTCATGCATGATGCTGTTTTTTGGGAGAGCTCTGGGGGTC 414
Qy 301 TGGGGAACAACATCATTCATCAGCACAGGTTCAATTTTTTCCCTGAAACACCTCGGTTCTCAG 360
Db 415 TGGGGAACAACATTTACCAGCACAGGTTTAATTTTTTCCCTGAAACACCTCGATCTCAG 474
Qy 361 CATGGGGACAAGTGGGTCTCAAGGTGACAGACCCAGAGCTCAGCTCTCCCCAGCA 417
Db 475 CATGGGGACAAGTGGGTCTCAGGGGACAGACGCTCAGAGCTCAGCTTATGGAGCA 531

RESULT 94
BM772351
LOCUS
DEFINITION K-EST0056477 S4SNU181 Homo sapiens cDNA clone linear EST 04-MAR-2002
            694 bp mRNA
mRNA sequence.
ACCESSION
VERSION BM772351
KEYWORDS BM772351.1 GI:19101966
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 694)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 1 row: B column: 07
High quality sequence stop: 694.
Location/Qualifiers
1..694
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="S4SNU181-1-B07"
/clone_lib="S4SNU181"
/sex="M"
/tissue_type="Stomach"
/cell_type="Lymphoblast-like"
/lab_host="Top10F"
/notes="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
inact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
combined cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
sequencing about 2,000 ~ 3,000 colonies in original cDNA
library, the abundant cDNAs were selected and amplified by
PCR reaction using vector region primer including T7

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promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells *E. coli* Top10F<sup>+</sup> with electroporation method."

```

BASE COUNT      162 a  222 c  189 g  120 t      1 others
ORIGIN

Query Match      16.4%; Score 333; DB 14; Length 694;
Best Local Similarity 100.0%; Pred. No. 4.6e-61;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  400 GCTCAGCCTCTCCACGACAGCCGCCAGCTTTGGCTCAACCGAGTATCAGAGCCCTCAG 459
Db   362 GCTCAGCCTCTCCACGACAGCCGCCAGCTTTGGCTCAACCGAGTATCAGAGCCCTCAG 421

QY  460 CAGCCACCCAGACCCGCTGGTGGTCCACGCAACAGAAACCGCGGTTTGGGCGAGGC 519
Db   422 CAGCCACCCAGACCCGCTGGTGGTCCACGCAACAGAAACCGCGGTTTGGGCGAGGC 481

QY  520 GGAGGGGCTGGCAGCGATAGCAACTCTCTCTGGAAGCGTCCAGGCTAATTCTGCCCCAGC 579
Db   482 GGAGGGGCTGGCAGCGATAGCAACTCTCTCTGGAAGCGTCCAGGCTAATTCTGCCCCAGC 541

QY  580 GTCGAATCCACCCGCTCTTGAAGAACTGAAGCTGCTCAGAGCTACACCCGGAAGAG 639
Db   542 GTCGAATCCACCCGCTCTTGAAGAACTGAAGCTGCTCAGAGCTACACCCGGAAGAG 601

QY  640 TTTGAGTGAATCTGAAGCGGCGGTCTTCATCATCAAGAGTACTCTGAGGAGCAG 699
Db   602 TTTGAGTGAATCTGAAGCGGCGGTCTTCATCATCAAGAGTACTCTGAGGAGCAG 661

QY  700 ATCCACCGCTCCATTAAAGTACTCATCTGGTGT 732
Db   662 ATCCACCGCTCCATTAAAGTACTCATCTGGTGT 694

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RESULT 95
BM748094      505 bp  mRNA  linear  EST 04-MAR-2002
LOCUS      K-EST0022789 SSSNU484 Homo sapiens cDNA clone SSSNU484-20-G06 5',
DEFINITION  mRNA sequence.
ACCESSION  BM748094
VERSION    BM748094.1 GI:19077712
KEYWORDS   EST.
SOURCE     human.

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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 505)
Kim.N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yusong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 20 row: G column: 06
High quality sequence stop: 505.
Location/Qualifiers
1. 505
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/db_xref="taxon:9606"

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FEATURES
source

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/clone="SSSNU484-20-G06"
/clone_lib="SSSNU484"
/sex="M"
/tissue type="Stomach"
/cell type="Epithelial"
/cell_line="SNU-484"
/lab_host="Top10F"

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/note="Organ: Stomach; Vector: pTZ18RP1; Site\_1: EcoRI; Site\_2: NotI; The poly (A)+ RNA was decapped with tobacco acid pyrophosphatase (TAP) and ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with *E. coli* DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells *E. coli* Top10F<sup>+</sup> by electroporation method."

```

BASE COUNT      124 a  171 c  129 g  81 t
ORIGIN

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Query Match      16.4%; Score 332; DB 14; Length 505;
Best Local Similarity 100.0%; Pred. No. 7.7e-61;
Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  400 GCTCAGCCTCTCCACGACAGCCGCCAGCTTTGGCTCAACCGAGTATCAGAGCCCTCAG 459
Db   174 GCTCAGCCTCTCCACGACAGCCGCCAGCTTTGGCTCAACCGAGTATCAGAGCCCTCAG 233

QY  460 CAGCCACCCAGACCCGCTGGTGGTCCACGCAACAGAAACCGCGGTTTGGGCGAGGC 519
Db   234 CAGCCACCCAGACCCGCTGGTGGTCCACGCAACAGAAACCGCGGTTTGGGCGAGGC 293

QY  520 GGAGGGGCTGGCAGCGATAGCAACTCTCTCTGGAAGCGTCCAGGCTAATTCTGCCCCAGC 579
Db   294 GGAGGGGCTGGCAGCGATAGCAACTCTCTCTGGAAGCGTCCAGGCTAATTCTGCCCCAGC 353

QY  580 GTCGAATCCACCCGCTCTTGAAGAACTGAAGCTGCTCAGAGCTACACCCGGAAGAG 639
Db   354 GTCGAATCCACCCGCTCTTGAAGAACTGAAGCTGCTCAGAGCTACACCCGGAAGAG 413

QY  640 TTTGAGTGAATCTGAAGCGGCGGTCTTCATCATCAAGAGTACTCTGAGGAGCAG 699
Db   414 TTTGAGTGAATCTGAAGCGGCGGTCTTCATCATCAAGAGTACTCTGAGGAGCAG 473

QY  700 ATCCACCGCTCCATTAAAGTACTCATCTGGTGT 731
Db   474 ATCCACCGCTCCATTAAAGTACTCATCTGGTGT 505

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RESULT 96

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AA361068
LOCUS

```

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DEFINITION

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ACCESSION

```

```

VERSION

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KEYWORDS

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SOURCE

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ORGANISM

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Homo sapiens

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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1 (bases 1 to 341)

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Adams,M.D., Karlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

```

```

,C.J., Lee,N.H., Kirkness,E.F., Weinschenk,K.G., Gockayne,J.D., White

```

```

,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,

```

```

Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

```

```

,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodok,A.,

```

```

Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,

```

```

Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,

```

```

Moreno-Palanco,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

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Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

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AA361068      341 bp  mRNA  linear  EST 21-APR-1997
EST70314 T-cell lymphoma Homo sapiens cDNA 5' end, mRNA sequence.

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AA361068
ACCESSION

```

```

VERSION

```

```

KEYWORDS

```

```

SOURCE

```

```

Homo sapiens

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

1 (bases 1 to 341)

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```

Adams,M.D., Karlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

```

```

,C.J., Lee,N.H., Kirkness,E.F., Weinschenk,K.G., Gockayne,J.D., White

```

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,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,

```

```

Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

```

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,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodok,A.,

```

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Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,

```

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Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,

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Moreno-Palanco,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

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Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

```





insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

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BASE COUNT      211 a  151 c  168 g  165 t
ORIGIN
Query Match      16.0%; Score 323.6; DB 12; Length 695;
Best Local Similarity 76.0%; Pred. No. 4.7e-59;
Matches 41; Conservative 0; Mismatches 129; Indels 1; Gaps 1;
Qy 583 GAATCCCAACCCCGCTCTTGAAGAACTGAAGCTGCTCAGACTCAACCCGAAAGAGTTT 642
Db 33 GAACCCCAACCCAGTGTGGAGAGCTTCGGTCCATTAACTATAACCCCAAGATTTT 92
Qy 643 GAGTGGAACTGAAAGCGCGGTGTTCATCATCAAGACTACTCTGAGAGACATC 702
Db 93 GACTGGAATCTGAAACATGCGCGGGTTTCATCATTAAGAGCTACTCTGAGGACGATAT 152
Qy 703 CACCGCTCCATTAAAGTACTCTGTTGTAGCAGACGCGCAACAAGCGCTGGAC 762
Db 153 CACCGTCCATTAAAGTATAATTTGGTGCAGCAGAGCATGGTAACAAGAGACTGGAT 212
Qy 763 AGCGCTTCCGCTGCATGAGCAGCAAGGGCCCGCTCTACCTGCTCTTCCAGCGTCAATGGG 822
Db 213 GCTGCTTATCGTTCCATGAACGGGAAAGGCCCGTTTACTTTTTCAGTGTCAACGGC 272
Qy 823 AGTGGGCAATTTTGTGGGTGGCGAGATGAAGTCCCGCTGGACTACGGCACCAGTGCC 882
Db 273 AGTGGACACATTTCTGTGGCGTGGCAGAAATGAATCTGCTGTGGACTACAAACACATGTGCA 332
Qy 883 GGGGTCTGCTCAGGACAACTGGAAGGGGAAGTTTGATGTCAGTGGATTTTGTGAAG 942
Db 333 GGTGTGTGTCCTCCAGGCAAAATGGAAGGGTC-GTTTGTATGTGAGTGGATTTTGTGAAG 391
Qy 943 GATGTATCCCAATAACCAAGCTCCGGCACATCAGGTGGGAGAAATAACGAAACCCGGTC 1002
Db 392 GACGTTCCCAATAGCAACTCGGACACATTCGCTAGAGAACACGAGAAATAAACCAAGT 451
Qy 1003 ACAAACTCCGGGACACCCAGGAGGTGCCCTTAGAAAAGCAAGCAAGTCTGAAATTT 1062
Db 452 ACCAACTCTAGGACACTCAGGAAAGTGCCTCTGGAAGAGGCTTAAGCAGGTGTTGAAATTT 511
Qy 1063 ATCAGTTCTTCAAGCACACAACTCCATCTTCCAGCAGCTTTGCTCACTACGAGAAGCGC 1122
Db 512 ATGCCAGCTACAGCACCACTCCATTTCCATTTTGTATGACTTCTCACACTATGAGAAACGC 571
Qy 1123 CA 1124
Db 572 CA 573
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RESULT 100
LOCUS      AL774891
DEFINITION AL774891 XGC-gastrula Silurana tropicalis cDNA clone TGas080113 5',
            mRNA sequence.
ACCESSION  AL774891
VERSION     AL774891.1 GI:21560595
KEYWORDS    EST.
SOURCE      western clawed frog.
            Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
            Xenopodinae; Silurana.
            1 (bases 1 to 654)
            Taylor, R., Ashurst, J.L., Croning, M.D.R., Zorn, A.M. and Rogers, J.
            Sanger Xenopus tropicalis EST project 2002
            Unpublished (2001)
            Contact: Taylor R
            Sanger Centre
            Hinxton, Cambridgeshire, CB10 1SA, UK
```

Email: trop@sanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS SEQUENCE ID: TGas080113.plkSP6  
Sequencing primer: PlkSP6  
This sequence is from a Xenopus Gene Collection (XGC) library  
constructed by Aaron M. Zorn.

## FEATURES

## Location/Qualifiers

1..654

/organism="Silurana tropicalis"

/db\_xref="taxon:8364"

/clone="TGas080113"

/dev\_stage="XGC-gastrula"

/lab\_host="Escherichia coli X11-blue"

/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA

was oligo dT primed from 5' end of poly A+ RNA from atages

10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated

into pCS107 with EcoRI at the 5' end and NotI at the 3'

end."

BASE COUNT 152 a 229 c 175 g 98 t

ORIGIN

Query Match 15.9%; Score 322.4; DB 9; Length 654;

Best Local Similarity 80.9%; Pred. No. 8.6e-59;

Matches 390; Conservative 0; Mismatches 86; Indels 6; Gaps 1;

Qy 436 CAACCGCAGTATCAGAGCCCTCAGCAGCCACCCAGACCGCTGGGTGCCCCACGCAAC 495

Db 179 CCACCGCCCTCAGCAGAGCCACAGGCCCTCAGAACCGCTGGGTGCCCCACGCAAC 238

Qy 496 AGAAACCGCGGTTTGGGCGAGCGGAGGGCTGGCGGATCAAACTCTCTCTGGAAAC 555

Db 239 AGGAACCTGCTTACGCCAGGGCGGA-----GGCCCCGACGGGAACCTCTCTGGCGGG 292

Qy 556 GTCAGCTCAATTTCTGCCCCAGCGTCAATCCACCCCGCTCTTGAAAACACTGAAAGCT 615

Db 293 GCTCAGTCTCACTCCGCCCTGGGAACGAGTCCACCCCGCTGGGAGAACTGAAAGCC 352

Qy 616 GTCACAGCTACAAACCGAAAGAGTTTGGTGGAACTCTGAAAAGCGGCGTGTTCATC 675

Db 353 GCCCAGAGCTACAAACCGAAAGAGTTTGGTGGAACTCTGAAAAGCGGCGTGTTCATC 412

Qy 676 ATCAAGAGCTACTCTGAGGACGACATCCACCGCTTCCATTAAGTACTCCATCTGTGTAGC 735

Db 413 ATAAAGAGCTACTCCGAGGACGACATCCACCGCTTCCATTAAGTACTCCATCTGTGTAGC 472

Qy 736 ACAGAGACGGCAACAGCGCTGGACAGCGCTTCCGCTGCATGAGCAGCAAGGGGCC 795

Db 473 ACAGAGACGGCAACAGCGCTGGATAGCGCTTCCGCTTCCATTAAGTACTCCATCTGTGTAGC 532

Qy 796 GTCTACCTGCTTTCAGCGTCAATGGGAGTGGGCAATTTTGTGGGTGGCGGAGATGAAG 855

Db 533 GTCTACCTTCTGTTTCAGCGTCAACGGGAGGAGACCTTCTGCGCGGTGGCGGAGATGAAG 592

Qy 856 TCCCGCGGTGGAAGTACGGCAACAGTGGCGGGGTCTGGTCTCAGGACAAAGTGAAGGGGAAG 915

Db 593 TCCCGCGGTGGAAGTACGGCAACAGTGGCGGGGTCTGGTCTCAGGACAAAGTGAAGGGGAAG 652

Qy 916 TT 917

Db 653 TT 654

Search completed: March 24, 2003, 01:13:56

Job time : 3534 secs

T., Waterston, R. and Wilson, R.  
WashU-Merck EST Project 1997  
Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@waterston.wustl.edu  
This clone is available royalty-free through LBNL; contact the  
IMAGE Consortium ([info@image.lbnl.gov](mailto:info@image.lbnl.gov)) for further information.  
Insert length: 831 Std Error: 0.00  
Seq primer: -41m13 fwd. ET from Amersham  
High quality sequence stop: 436.

## FEATURES source

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/clone="IMAGE:727735"  
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/sex="male"  
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macia) polylinker. Site 1: SfiI  
was prepared from mRNA obtained  
inc... and primed with a NotI  
TGTTACCAATCTGAATGGGAGCGCGCGC  
Double-stranded cDNA was ligat  
(Pharmacia), digested with NotI  
and Eco RI sites of the modified  
went through one round of normal  
constructed by Bento Soares a

	BASE COUNT	ORIGIN
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100	0.000	0.000

Query Match	13.5%	Score 274;	DB 1;	Length 447;
Best Local Similarity	100.0%;	Pred. NO. 3.7e-59;		
Matches 274;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1755	TTTGAANAATCTTTCCTTCCAGATCTGTTGCCACCTGAACAGCCACCCCTGTCCTCACTGTC	1814		
Db 1	TTTGAANAATCTTTCCTTCCAGATCTGTTGCCACCTGAACAGCCACCCCTGTCCTCACTGTC	60		
1815	CTGCTGTCCGATTTGGGCTGGATGGTTTGGGCGATGATGTGTGGAGGAACCTGGAGGGTGC	1874		
61	CTGCTGTCCGATTTGGGCTGGATGGTTTGGGCGATGATGTGTGGAGGAACCTGGAGGGTGC	120		
1875	TTTAAAGTCTGGTTCAGGGTTCGGGCATCTTCTGTTGTTCGACATCTTTTAAATTTTACA	1934		
Db 121	TTTAAAGTCTGGTTCAGGGTTCGGGCATCTTCTGTTGTTCGACATCTTTTAAATTTTACA	180		
1935	CCCTTTCTTAAGAAATCTAATGCCGCTTAAGTTTTTTTATACCAATAATGCTGAGCTTTAA	1994		
Db 181	CCCTTTCTTAAGAAATCTAATGCCGCTTAAGTTTTTTTATACCAATAATGCTGAGCTTTAA	240		
1995	GTGTAGGATCTGGTAGTACAGACAGTGTGATGGA	2028		
241	GTGTAGGATCTGGTAGTACAGACAGTGTGATGGA	274		*

RESULT	68
AW641341	
LOCUS	553 bp mRNA linear EST 26-APR-2001
DEFINITION	cm06d01.wl Blackshrew/Soare's normalized Xenopus egg library Xenopus laevis cDNA clone PX0105D01 5', mRNA sequence.
ACCESSION	AW641341
VERSION	AW641341.1 GI:7398599
KEYWORDS	EST African clawed frog.
SOURCE	Xenopus laevis
TISSUE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

REFERENCE  
AUTHORS

[illegible]

Contact: Perry J. Blackshear  
 Office of Clinical Research and Laboratory of Signal  
 Transduction  
 National Institute of Environmental Health Sciences  
 1A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709  
 USA  
 Tel: 919 541-4899  
 Fax: 919 541-4571  
 Email: black009@niehs.nih.gov  
 Clone is available through Research Genetics, Inc., 2130 Memorial  
 Parkway, Huntsville, AL 35901  
 phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email  
 cdna@resgen.com  
 DNA sequencing and analyses performed by National Institutes of  
 Health Intramural Sequencing Center (NISC).

PCR primers  
FORWARD: TGTAAACGACGGCCAGT

FORWARD: TGGTCTGTTTG  
BACKWARD: CAGGAACAGCTATGACC  
Plate: 0105 row: D column: 01  
seq primer: T7 primer.

## FEATURES

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/db_xref="taxon:8355"
/clone="PX0105D01"
/clone_lib="Blackshear/Soares normalized Xenopus egg
library"
/sex="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
/notes="Vector: pTTT3-Pac; Site_1: EcoRI; Site_2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
pTTT3-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subtraction: two
approaches to facilitate gene discovery', Genome Research
6:791-806, 1996. The first strand synthesis used a
NotI-drf18 primer: double stranded cDNAs were ligated to
EcoRI adapters, digested with NotI, and directionally
cloned into the NotI and EcoRI-digested pTTT3-Pac vector.
The library contained approximately 7.2 X 105
recombinants, with average insert sizes of 1-1.5 kb."
155 g 125 g 134 t

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100	0	0

	Query Match	13.5%;	Score 273;	DB 2;	Length 553;
	Best Local Similarity	78.4%;	Pred. No. 7e-59;		
	Matches 327;	Conservative	0;	Mismatches 90;	Indels 0; Gaps
QY	1	CAAAAGCA	AGATAT	AAAGTACAA	ATGGTTCTGTATTACATCAGAAGGATACAGGTTCAATG 60
DB	33	CAAAACAATGATCTATTATTCAGTTTCANAA	CGGATCCCTGCTCATCAGAAGCACAGCGTGCACG 92		
QY	61	ACAATGACTTTTGAGCCCTACCTTATCTGGACAGTC	CAAAATCAGAGTAACAGGTTTACCCCTCAA 120		
DB	93	ATAATGACTTTTGAGCAGTACCTGTGCGGGGAGCTCCAT	CAGAGTAAACAGCTACCCCTTCCA 152		
QY	121	TGACGACCCCTCCTCTGTCCAGCTTAATACCGCCGTC	CAATTGGATTTCTTACTTCTCTCA 180		
DB	153	TGACAGACCCCTTATCTATCCAGTTACTACCCCTCTCTT	ATTGGCTTTTCGTTATTCCTCTCA 212		
QY	181	ATGAGGCTCCGTGCTTACTGACGGGACCCCTCGGATTTCC	ATCTACCTCACCTACGGAC 240		



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 /tissue\_type="pooled germ cell tumors"  
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 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; let strand cDNA was prepared from 3 pooled  
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 oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
 RI adaptors (Pharmacia) digested with Not I and cloned  
 into the Not I and Eco RI sites of the modified pT73  
 vector. Library is normalized. Library was constructed by  
 Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT 169 a 162 c 133 g 215 t  
 ORIGIN

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 Best Local Similarity 74.0%; Pred. No. 1.2e-61;  
 Matches 37; Conservative 0; Mismatches 130; Indels 1; Gaps 1;  
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 Db 679 TTATCATTAAGAGTCTCTGAGGACGATATTTTACCGTTCATTAAGTATTAATTTGG 620  
 QY 730 TGTAGCAGAGCAGCGCAACAGCGCTTGACAGCGCTTCCGCTGCATGAGCAGCAAG 789  
 Db 619 TGCAGCAGCGGACATGTAACAGAGACTGATGCTGCTTATCTTTCATGAACGGGAAA 560  
 QY 790 GGGCCCTCTACCTCTCTTACAGGTCAATGGAGTGGGCTTTTGTGGGGTGGCCGAG 849  
 Db 559 GGGCCCTTTACTTACTTTTTCAGTGTCAACCGCAGTGGACACTTCTGTGGCGTGGCAGAA 500  
 QY 850 ATGAAGTCCCGGTGGACTACGGCAGCAGTCCCGGCTTGGTCTCAGGACAGTGAAG 909  
 Db 499 ATGAATCTGCTGAGCTACACATGTCAGGTGTGGTCCCGAGCAATGGAAG 440  
 QY 910 GGAAGTTTCAATGCTCAGTGGATTTTGTAAAGATGTACCATTAACAGCTCCGCGAC 969  
 Db 439 GGTGCTTTTGTATGCTCAGTGGATTTTGTGAGGACGTTCCCATAGCAACTGGGACAC 380  
 QY 970 ATCAGCTGAGATACGACCAACACCGGTCAAACTCCCGGGACACCCAGGAGGTG 1029  
 Db 379 ATTGGCTAGAGAACACAGAGATAAACAGTGAACCACTCTAGGAGACACTCAGGAAGTG 320  
 QY 1030 CCCTTAGAAAAGCCAGCAAGTGTGTAATTTATCATGTTCTTACAGACACACACTCC 1089  
 Db 319 CCTCTGAAAAGGCTAAGCAGGTGTGTAATTTATAGCCAGCTACAGACACACTTCC 260  
 QY 1090 ATCTTCGACGACTTCTCCTACATGAGAGAGCGCC-AGAGGAGGAGGAGTGTGCCAG 1149  
 Db 259 ATTTTGTGATGACTTCTCAGACTATGAGAGAGCGCCAGAGAGAGAGAGAGAGTGTAAAG 200  
 QY 1149 GAACGACAGTGCAGAACAAACAA 1172  
 Db 199 GAACGTCAGGTGCTGGGAATAA 176

RESULT 66  
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 VERSION AL627746.1 GI:16597229  
 KEYWORDS EST.  
 SOURCE western clawed frog.  
 ORGANISM Silurana tropicalis

REFERENCE  
 AUTHORS Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.  
 TITLE Sanger Xenopus tropicalis EST project 2001 (10\_2001)  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Huckle E

Sanger Centre  
 Hinxton, Cambridgeshire, CB10 1SA, UK  
 Email: tropesanger.ac.uk  
 Sanger Xenopus tropicalis EST project 2001  
 TROPICALIS SEQUENCE ID: TGAs025h05.sp6  
 Sequencing primer: Sp6  
 This sequence is from a Xenopus Gene Collection (XGC) library  
 constructed by Aaron M. Zorn.

FEATURES  
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 10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated  
 into pCSI07 with EcoRI at the 5' end and NotI at the 3'  
 end."

BASE COUNT 139 a 253 c 166 g 129 t 2 others  
 ORIGIN

Query Match 13.6%; Score 274.8; DB 1; Length 689;  
 Best Local Similarity 79.4%; Pred. No. 2.6e-59;  
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 QY 1 CAAAGGACAGATAATAAGTACAAATGGTTGTTACATCAGAGGATACAGTTTCATG 60  
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 QY 61 ACATGACCTTGGACCTTACCTTACCTGACAGTCAATCAGAGTAAACAGTTACCCCTCAA 120  
 Db 303 ATATGACTTCGAGCAGTACTCTGCGGACAGTCCCAATCAGAGTAAACAGTTACCCCTCAA 362  
 QY 121 TGAGGACCCCTAGCTGCTCAGCTATACCGCGCTTCATTTGAGTTCCTTACTCCCTCA 180  
 Db 363 TGACGACCCGCTACCTGCTCAGTTACTACCTCTTCTATCGGCTTTCGTTATTCGCTCA 422  
 QY 181 ATGAGCTCCGCTGCTTACTGCGAGGAGCCCTCCGATTCATACCTCACCACCTACGGAC 240  
 Db 423 GCGAGCTCTTGGTCAACCGCGGGGACCCCGGATCCGTTACCTCACCCTGACGGAC 482  
 QY 241 AGCTGATGACGGAGACCATCAATTTTATGACAGTCTGTTTTGGGAGCCTTGGGGGCC 300  
 Db 483 AGCTGACGACGGAGACCATCAATTTTATGACAGTCTGTTTTGGGAGCCTTGGGGGCC 542  
 QY 301 TGGGGAACAACATCTATCAGCAGAGTTCAATTTTTCCTGAAAACCTCGGTTCTCAG 360  
 Db 543 TGGGAATAACATCTATCAGCAGCGGTTCACTTCTCCCGGAAAACCCAGCCTTTTCG 602  
 QY 361 CATGGGGGACAGTGGGTCTCAAGTCTCAGAGCAGACCCAGAGCTCAGCCT 408  
 Db 603 CATGGGGGACAGCGGCTCCGAGGGGACAGACCCAGAGCTCCGCT 650

RESULT 67  
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 ACCESSION AA398704  
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 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,  
 Schellenberg, K., Steptoe, M., Tan, P., Theising, B., White, Y., Wyllie



/lab host="DH10B"  
/notes="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from pooled 8-9 week  
(total) fetus material with a Not I - oligo(dT) primer [5'  
TGTTCAATCTCAAGTGGAGGGCGGCTTAATTTTCTTTTCTTTT  
TGTACAACTCAAGTGGAGGGCGGCTTAATTTTCTTTTCTTTTCTTTT  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT	85 a	104 c	97 g	59 t
ORIGIN				
Query Match	16.6%	Score 336.8	DB 9	Length 355
Best Local Similarity	99.1%	Pred. No. 7.4e-62		
Mismatches	349	Conservative	0	Mismatches 2; Indels 1; Gaps 1
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Db	5	CGGAGGGCTGGCAGGATA-CAACTCTCTCGGAAACGTCGAGCTAATTTCTGCCCCAG	63	
Qy	579	CGTCAATCCACCCCGCTTGAATACTGAAGCTGCTCACAGTACCAACCCGAAAGA	638	
Db	64	CGTCAATCCACCCCGCTTGAATACTGAAGCTGCTCACAGTACCAACCCGAAAGA	123	
Qy	639	GTTCAGTGGAACTCAAAAGCGGGCTGTGTTTCATCATCAAGAGTACTCTGAGGAGA	698	
Db	124	GTTCAGTGGAACTCAAAAGCGGGCTGTGTTTCATCATCAAGAGTACTCTGAGGAGA	183	
Qy	699	CATCCACCGCTCCATTAAGTACTCCTATCTGTTAGCAGACGCGGCAACAGCGCT	758	
Db	184	CATCCACCGCTCCATTAAGTACTCCTATCTGTTAGCAGACGCGGCAACAGCGCT	243	
Qy	759	GGACAGCGCTCCGCTGATGAGCAGGAGGGCGGCTCTACTCTCTTCAAGCGTCAA	818	
Db	244	GGACAGCGCTCCGCTGATGAGCAGGAGGGCGGCTCTACTCTCTTCAAGCGTCAA	303	
Qy	819	TGGAGTGGGCAATTTTGTGGGTGGCGGAGATGAAGTCCCGTGGACTAC	870	
Db	304	TGGAGTGGGCAATTTTGTGGGTGGCGGAGATGAAGTCCCGTGGACTAC	355	

RESULT 87  
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AGENCY 8753787 NIH\_MGC\_130 Mus musculus cDNA clone IMAGE:6393617  
5', mRNA sequence.  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: gnapbs-rc@mail.nih.gov  
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,  
Ph.D.  
CDNA Library Preparation: ResGen, Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
Sequencing by: Agencourt Bioscience Corporation  
Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://img.llnl.gov  
row: f column: 18  
sequence stop: 741.  
qualifiers

/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone="IMAGE:6393617"  
/clone\_lib="NIH\_MGC\_130"  
/lab host="DH10B (phage-resistant)"  
/note="Organ: oocytes; Vector: pCMV-Sport6.1.cdbd;  
Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally.  
Primer: Oligo dT. Average insert size 1.95 kb.  
Constructed by ResGen, Invitrogen Corp. Note: this is a  
NIH\_MGC Library."

BASE COUNT	261 a	222 c	242 g	205 t	7 others
ORIGIN					
Query Match	16.6%	Score 336.2	DB 14	Length 937	
Best Local Similarity	74.7%	Pred. No. 9.1e-62			
Mismatches	422	Conservative	0	Mismatches 143	Indels 0; Gaps 0
Qy	583	GAATCCACCCCTCTCTGAAAGCTGAAGCTGCTCACAGCTACACCCGGAAGATTTT	642		
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Qy	643	GAGTGGATCTGAAGCGGGCTGTGTTTCATCATCAAGAGTACTCTGAGGAGCATC	702		
Db	352	GAGTGGATCTGAAGCAATGCGCGGGTTTTTCATCATTAAGAGTACTCTGAGGAGCATC	411		
Qy	703	CACCGCTCCATTAAGTACTCATCTGCTGTAGCAAGAGCGGCAACAGCGCTGAC	762		
Db	412	CACCGTCCATTAAGTATAATCTGCTGAGCAGCAGAGCATGCTAACAGAGACTGGAT	471		
Qy	763	AGCGCTTCGCTGATGAGCAGCAAGGGCGGCTCTACTGCTCTTCAGCGTCAATGG	822		
Db	472	CGCGCTATCTGCTGATGAGGAGGGTCCGCTGCTACTTCTTTCAGTGTCAACGGC	531		
Qy	823	AGTGGGCAATTTTGTGGGTGGCGGAGTGAAGTCCCGTGGACTACGGACCAAGTGC	882		
Db	532	AGTGGGCAATTTTGTGGGTGGCGGAGTGAAGTCTGCTGGAGTACACACATGTGCA	591		
Qy	883	GGGTGCTGCTCTCAGGACAACTGGAAGGGGAGTGTGATGCTCCAGTGGATTTTGTAG	942		
Db	592	GGTGTGCTGCTCCAGGACAACTGGAAGGGTCTGTTTCGATGTCAGATGATTTTGTGAG	651		
Qy	943	GATGTACCAATAACCACTGCGGCAATCAGGCTGGAGATTAAGCAACAAACCGGTC	1002		
Db	652	GAGTGTCCCAATAGCCAACTGCGACATTCGTCTAGAGAACACGAGATTAACCGATG	711		
Qy	1003	ACAACTCCGCGGACACCCAGGAGTGCCTTAGAAAAGCCCAAGCAAGTGTGAAAATTT	1062		
Db	712	ACCAACTCTAGGACACTCAGGAGTGCCTCTGGAAGAAAGCTAGCAGGTGTTGAAAATC	771		
Qy	1063	ATCAGTTCCTACAGCAGCAACACCTCCACTTCTTCGAGACTTTGCTCATTCCAGAGCGC	1122		
Db	772	ATAGCCAGCTACAGCAGCAACCACTTCCATTTTGTGAGACTTCTCAGACTATGAGAACGC	831		
Qy	1123	CAGAGGAGGAGGAGTGGTGGCGAA	1147		
Db	832	CAAGAGGAGGAGGAGTGGTGGTAA	856		

RESULT 88  
BJ063156  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
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BJ063156 NTBB Mochii normalized xenopus tailbud library Xenopus  
laevis cDNA clone XL070e20 5', mRNA sequence.  
EST.  
BJ063156  
BJ063156.1 GI:17422181  
African clawed frog.  
Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
Xenopodinae; Xenopus.  
1 (bases 1 to 719)  
Kitayama, A., Terasaka, C., Mochii, M., Veno, N., Shin-i, T. and Kohara

409 CATCAAGTACTCTATCTGGTGTACTCTGAGCATGGTAATAGGGTTGGATGCA  
 825 GCCTCCGCTGCATGAGCAGCAAGGGGCCGCTCTACTCTCTTCAGCGGTCAATGGGAGT  
 408 GCTTACCGTTCCCTCAATGGGAAGGCCACTCTATTGCTCTTCAGTGTGATGGCGAGT 349  
 886 GGGCAATTTTGTGGGGTGGCCGAGATGAAGTCCCCCGTGGACTACGGCACCAGTGCCTGGG  
 348 GGACATTTTGTGTGGAGTGGCTGAATGAAGTCTGTGTAGACTATAATGCTTATGCTGGT 289  
 886 GTCTGGTCTCAGGACAACTGGNAGGGGAACTTTGATGTCCAGTGGATTTTGTTAAGAT 945  
 288 GTTTGGTCTCAGGATAAATGGNAGGGCAATTTGAAGTTAAATGATCTTTGTCAAGAT 229  
 946 GTACCCAATACCAGCTCCGGCACAATCAGGCTGGAGATTAACGACACAAACCCGTACA 1005  
 228 GTTCCCAATACCAGATTAACGACATATTCGTTAGAAAATATGACACAAACCGATACC 169  
 1006 AACTCCCGGGCACCCAGGAGTGCCCTTAGAAAAGCCAGCAGTGCTGAAAATTATC 1065  
 1006 ATTCAAGAGACATCAAGAGTACCCCTAGAAAAGCAAGCAAGTGCTTAAATAATTT 109  
 1006 AGTTCTCTTCAAGACACAACTCCATCTTTGACGACTTTGTCTCACTACGGAAGCG-CCA 1124  
 108 GCTACTTTCAAGCACCACTCAATCTTTGATGACTTTCACATTTATGAAGCGGTCAA 49  
 1125 GAGGAGGAGGAGTGGTCCGCAAGGAA 1151  
 48 GAGGAGGAGGAGGCGCATCGCAAGGATA 22

**SOURCE**

AL515909 LTI\_NFL011\_NBCL Homo sapiens cDNA clone CS0DA001YB18  
prime, mRNA sequence.

AL515909 AL515909 GI:12779402 EST.  
human.

**TISSUE**

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 917)

Li,W.B., Gruber,C., Jesse,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
Contact : Genoscope

**ORGANISM**

Genoscope - Centre National de Sequencage  
BP 191 9106 EVRY cedex - France  
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

1..917

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0DA001YB18"  
/clone\_lib="LTI\_NFL011\_NBCL"  
/sex="male"  
/tissue\_type="neuroblastoma cells"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMWSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMWSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

174 a 274 c 228 g 206 t 35 others

COUNT

ORIGIN  
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 Best Local Similarity 98.8%; Pred. No. 3.8e-62;  
 Matches 366; Conservative 17; Mismatches 27; Indels 2; Gaps 2;  
 Qy 1 CAAAAGGACAGATAATAAGTACAAAATGGTTCGTTACATCAGAAGGATACAGTTCATG 60  
 Db CAAAAGGACAAATAATAATTTTACAAAATGGTTCGTTACATCATAAGGATATATTCATT 337  
 Qy 61 ACAATGACTTTGAGCCCTACCTTACCTGGACAGTCAAAATCAGAGTAAAGTACCCCTCAA 120  
 Db AYAATTAATTTTAAKCYCTACTTACTGGACATTTAAATVAGATTACATTTACCCCTTAA 397  
 Qy 121 TGACGACCCCTACCTGTCAGGTATATCCCGCGGTCCATTGGATTTCTTACTCCCTCA 180  
 Db TTACTACCCCTACCTTTCAGGTATATTCGCGTTCATTTGGATTTCTTACTCCCTCA 457  
 Qy 181 ATGAGGCTCCGTG-GTCTACTGACGGGACCCCTCCGATTCACCTACCTACCCCTACGGA 239  
 Db ATGAGGCTCCGTGTCATTTCTGKATCCCTCCGATTCACCTACCTACCCCTACGGA 517  
 Qy 240 CAGCTCAGTAAACGAGACCATCATTTATATGACGATGCTGTTTTGGGAGCCCTGGGGC 299  
 Db CAGCTCAGTAAACGAGACCATCATTTATATGACGATGCTGTTTTGGGAGCCCTGGGGC 577  
 Qy 300 CTGGGGAACAACTCTATCAGCAGGTTCAATTTTTTCCTGAAAACCCCTGGTTCTCA 359  
 Db CTGGGGAACAACTCTATCAGCAGGTTCAATTTTTTCCTGAAAACCCCTGGTTCTCA 637  
 Qy 360 GCAT-GGGGGACAAAGTGGGTCTCAAGCTCAGCAGACCCAGAGCTCAGGCTCT 410  
 Db GCATGGGGGACAAAGTGGGTTCACAGCTCAGCAGACCCAGAGCTCGGCTAT 689  
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 LOCUS z65c02.r1 Soares total fetus Nb2HP8 9w Homo sapiens cDNA clone  
 DEFINITION IMAGE:796418 5' similar to TR:G849195 G849195 CHROMOSOME IV COSMID  
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 VERSION AA460050.1 GI:2184934  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 355)  
 AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,  
 Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin,J., Moore,B.,  
 Schellenberg,K., Stepec,M., Tan,F., Theising,B., White,Y., Wyllie,  
 T., Waterston,R. and Wilson.R.  
 WASHU-Merck EST Project 1997  
 Unpublished (1997)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -28ml3 rev2 Et from Amersham  
 High quality sequence stop: 325.  
 Location/Qualifiers  
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 FEATURES  
 source







promotor as 5' primer and N(dt)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA probes by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the substracted cDNA libraries were constructed by transfection of the remaining DNA into competent cells E. coli Top10F<sup>+</sup> with electroporation method."

ASE COUNT 162 a 222 c 189 g 120 t 1 others  
 Query Match 16.4%; Score 333; DB 14; Length 694;  
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 b 362 GGTGAGCTCTCCAGCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 421  
 Y CAGCCACCCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 519  
 b 422 CAGCCACCCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 481  
 Y 520 GGAGGGCTGGCAGGATAGCACTCTCTGGAAACGTCAGGCTTAATCTGCCCCCAGC 579  
 b 482 GGAGGGCTGGCAGGATAGCACTCTCTGGAAACGTCAGGCTTAATCTGCCCCCAGC 541  
 Y 580 GTGGAATCCACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 639  
 b 542 GTGGAATCCACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 601  
 Y 640 TTGAGTGGAAATCTGAAAGCGGGCGTGTCTCATCATCAGAGCTACTCTGAGGAGC 699  
 b 602 TTGAGTGGAAATCTGAAAGCGGGCGTGTCTCATCATCAGAGCTACTCTGAGGAGC 661  
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 b 662 ATCCACCGCTCCATTAAGTACTCAATCTGCTGT 694

RESULT 95  
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 OUR human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 505)  
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
 Kim, Y.S.  
 21C Frontier Korean EST Project 2001  
 Unpublished (2002)  
 CONTACT Contact: Kim YS  
 GENOME Genome Research Center  
 KOREA Research Institute of Bioscience and Biotechnology  
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 20 row: G column: 06  
 High quality sequence stop: 505.  
 Location/Qualifiers  
 1. 505  
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RESULT 96  
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 EST70314 T-cell lymphoma Homo sapiens cDNA 5' end, mRNA sequence.  
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 ACCESSION  
 VERSION  
 KEYWORDS EST.  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 341)  
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Feldner, R.A., Bult,  
 C.J., Lee, N.H., Kirkness, E.F., Weinatock, K.G., Gocayne, J.D., White,  
 O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,  
 Cline, T.R., Cotton, M.D., Barle-Hughes, J., Pine, L.D., Fitzgerald,  
 L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodok, A.,  
 Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,  
 Kelley, J.C., Liu, L.-I., Marra, S.M., Merrick, J.M., Moreno-Palauques, R.F.,  
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Fellgrino, S.M.,  
 Phillips, C.A., Ryder, S.B., Scott, J.L., Saudek, D.M., Shirley, R.,

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 Site 2: NotI; The poly (A)+ RNA was decapped with tobacco  
 acid pyrophosphatase (TAP) and ligated with DNA-RNA linker  
 including EcoRI site by treatment of T4 RNA ligase. The  
 first strand cDNA was synthesized from oligo dt-selected  
 mRNA by priming with dt-tailed vector. The dt-tailed  
 vector was adjusted to have about 60nt. The cDNA vector  
 was circularized with E. coli DNA ligase after digestion  
 of EcoRI which site is also included in vector. An RNA  
 strand converted to a DNA strand by Okayama-Berg method.  
 The obtained cDNA vectors were used for transfection of  
 competent cells E. coli Top10F<sup>+</sup> by electroporation  
 method."

BASE COUNT 124 a 171 c 129 g 81 t  
 Query Match 16.4%; Score 332; DB 14; Length 505;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-61;  
 Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 400 GGTGAGCTCTCCAGCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 459  
 Db 174 GGTGAGCTCTCCAGCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 233  
 QY 460 CAGCCACCCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 519  
 Db 234 CAGCCACCCAGACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 293  
 QY 520 GGAGGGCTGGCAGGATAGCACTCTCTGGAAACGTCAGGCTTAATCTGCCCCCAGC 579  
 Db 294 GGAGGGCTGGCAGGATAGCACTCTCTGGAAACGTCAGGCTTAATCTGCCCCCAGC 353  
 QY 580 GTGGAATCCACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 639  
 Db 354 GTGGAATCCACCCCGCTGGTGGTCCACGACGATATCAGAGCCCTCAG 413  
 QY 640 TTGAGTGGAAATCTGAAAGCGGGCGTGTCTCATCATCAGAGCTACTCTGAGGAGC 699  
 Db 414 TTGAGTGGAAATCTGAAAGCGGGCGTGTCTCATCATCAGAGCTACTCTGAGGAGC 473  
 QY 700 ATCCACCGCTCCATTAAGTACTCAATCTGCTGT 731  
 Db 474 ATCCACCGCTCCATTAAGTACTCAATCTGCTGT 505





